GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nuc	nucleic	: search, using sw model
Run on:	March	th 3, 2003, 21:30:10; Search time 4788 Seconds (without alignments) 10606.599 Willion cell updates/sec
Title: Perfect score: Sequence:	US- 174	US-10-017-621-3 1745 1 tygaagcagcglaaaggatggttcacctgcccacttgtcc 1745
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Searched:	205	2054640 seqs, 14551402878 residues ,
Total number of	hits	satisfying chosen parameters: 841850
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Postrprocessing:	¥ 8 3	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

REFERENCE AUTHORS TITLE JOURNAL

HSHCAK

HSHCAK

HSAPiens mRNA for Cdk activating kinase.

N 76171

X76171 GI:429096

S activating kinase.

Homo saptens.

Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Memalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RE i (bases 1 to 49)

RS Hall, F.L.

Direct Submitsed (08-NOV-1993) F.L. Hall, Childrens Hospital Los Angeles,

RESULT 1
HSHCAK
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Rose-John,S.
CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS
PALENT: NO 9732891-A 9 12-SEP-1997;
ANGEMANDTE GENTEANOLOGIE SYST (DE); ROSE JOHN STEFAN (DE)
LOCALLON/QUAILITIES
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Varbham, H.Karsenty. and Codowski, P.J.

Wethods and kits using macrophage stimulating protein

Patent: US 5696086-A 5 09-DEC-1997;
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Sequence 2780 from Patent WO0140521.
AXI59452 AXI59452.1 GI:14540783
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                                                                                                                                                                                                                                                                                                                 /organism="unidentified"
/db_xref="taxon:32644"
1 26 c 4 9
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Sequence 9 from Patent WO9732891.
A93722
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1 16 c 12 g
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Best Local Similarity 69.8%
Matches 30; Conservative
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Division of Orthopaedic Surgery, 4650 Sunset Boulevard, Los
Angeles, CA, 90027, USA
Gasses I to 49)
Wu.L. and Hall, P.L.
Unpublished
3 (bases I to 49)
Wu.L. Yee, L. Liu, L., Carbonaro Hall, D., Venkatesan, N., Tolo, V.T.
and Hall, F.L.
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Rose-John, S.
COMPIGATE FOR MODIFFING INTERACTIONS RETWEEN PROTEINS
PACENT: WO 9712891-A B 12-SEP-1997;
An. ARE'E CENTECHNOLOGIE SYST (DE): ROSE JOHN STEFAN (DE)
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
/db_xref="TaKC Bw":
/cell_line="Ew! Ewings sarcoma"
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/clouc_type="tumour"
/clouc_lib="rakC"
/lissue_type="tumour"
/clouc_lib="rakC"
                                                                                                                      Molecular cloning of the human CAKI gene encoding cyclin-dependent kinase-activating kinase cyclin-dependent kinase-2006 (1994)
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/product="protein kinase"
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/db_xref="G1:939888"
/db_xref="SPTREMBL:Q14495"
/translation=FRMSSKTGREMFGGIFW"
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/organism-"unidontified"
/db_xxcf-"taxon:32644"
/ a 4 c 26 g 13
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A93721
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Best Local Similarity 66.0%
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Reddy,v.S. and Sadhu,L.
Transplastcmic plants
Patent: WO 0206497-A 53 24-JAN-2002;
International Centre for Genetic Enginecring and Biotechnology (IT)
Location/Qualifiers
           Patent: WO 0142441-A 53 14-JUN-2001;
International Centre for Genetic Engineering and Biotechnology (IT)
Location/Qualifiers
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Edwards,C.A., Cantor,C.R., Andrews,B.N., Turin,L.H. and Fry,K.E. Method of determining DNA sequence preference of a DNA-binding molecule
Patent: US 5869241-A 156 09-FEB-1999;
Location/Qualifiers
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80.6%; Pred. No. 2.8e+06;
tlve 0; Mismatches 6;
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/organism="synthetic construct"
/db_xref="taxon:32630"
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/Organism-"synthetic construct"
/db_xref-"taxon:32630'
/note-"Primer"
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Sequence 156 from patent US 5869241.
AR032544
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Sequence 53 from Patent W00206497.
AX382049
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/organism="unknown"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamballa; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 31)
Carglll,M., Treland,J.S. and Lander,E.S.
Human single nucleotide polymorphisms
Patent; WO 016800-A 75.13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
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Mammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo. 1 (bases 1 to 50)
Shimkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
Patent: WO 014051-A 2780 07-JUN-2001;
Cutagen Corporation (US)
Location/Qualiflers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/note="Nucleotide deleted between bases 25 and 26
Accession number c942460243"
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1 (bases 1 to 42)
Reddy,S.1., Sadhu,L.I., Shukla,V.C. and Ferraiolo,G.I.
Plastid transformation
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Best Local Similarity 80.0%; Pred. No. 2.6c+06;
Matches 24; Conservative 1; Mismatches 5;
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Sequence 53 from Patent WO0142441.
AX182243
AX182243.1 GI:15133518
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/db_xref-"taxon:9606"
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AX248015
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Edwards.C.A., Cantor.C.R., Andrews, B.H., Turin, L.M. and Fry, K.E. Sequence-directed DNA-binding molecules compositions and methods Patent: US 557844-A 156 26-NOV-1996;
Location/Qualifiers
                                                                                                                                                                                                                                      1 (bases 1 to 46)
Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E. Sequence directed DNA binding molecules compositions and methods Patent: US 6384208 A 156 07-MAY-2002;
Location/Qualifiers
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Best Local Similarity 71.8%; Fred. No. 2.88+06; Matches 28; Conservative 0; Mismatches 11; Indels
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VERSION 190958.1 GI:3935428
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Eukaryota; Hetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 31)
Cargill, M., Ireland, J.S. and Lander, E.S.
Human single nucleotide polymorphisms
Patent: WO 0166800A, 94 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
Schlegel, R., Deeds, J., Berger, A. and Zhao, X.
Genes, compositions, kits, and methods for identification,
assessment, prevention, and therapy of cervical cancer
Patent: MO 043467-A 1933 14-JUN-2001;
Millennium Preddictive Medicine, Inc. (US)
Location/Qualifiers
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I (bases 1 to 46)
Edwards.C.R., Andrews,B.M. and Turin,L.M.
Screening assay for the detection of DNA-binding molecules
Patent: US 5726014-A 156 10-MAR-1998;
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Best Local Similarity 77.44; Pred. No. 3.5e+06;
Matches 24; Conservative 1; Mismatches 6; Indels
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Sequence 1933 from Patent WOO142467.
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Sequence 94 from Patent WO0166800.
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AX248015.1 GI:15862638
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Sequence 24 from Patent WO9910358.
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Minimum DB Maximum DB

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46 bp mRNA linear EST 28-JAN-1997 V71905.rl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMACE: 248216 5' similar to gb:x66363 SERINE/THREONINE-PROTEIN NT NR NS BCTAIRE (HUMAN); mRNA sequence. N78054 I GI:1240755
             BM997711 5009-0-35
AZ231355 100259104
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AZ291593 AU0259104
AZ29595 200268F0
AZ29155 AU0269F0
AZ39155 AU0268F0
AZ475974 L195506.x
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Eukaryota, Metazoa; Chordata; Craniata; Vortebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 46)
1 (bases 1 to 46)
1 (bases) Loudon, G., Becker, M., Bonaldo, M.F., Chlapelli, B.,
Chissoe, S., Dietrich, M., DuBuque, T., Pavello, A., Gish, W., Havkins,
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
B., Morris, M., Parsons, J., Pange, C., Riffin, L., Rohlfing, T.,
Schellenberg, K., Soares M. B., Ten, F., Thicrry-Meg, J., Trevaskis, E.,
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
Genome, Res. 6 (9), 807-828 (1996)
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BI910989 603069394
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
1314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
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AU104587
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TA1656050
AI250043
AZ966392
AU103382
AU103553
BI910989
AU105237
AE89393
AE311362
AU106960
AE3111536
AE311536
AE30601
AI475974
BH811451
W39000
AU104829
BG422154
AE450951
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AU103381
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T74703
AIS91257
AIS972479
BH98772479
BH98772479
BH987724
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AU103359
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Contact: Wilson RK
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N78054
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R38968 yd07c08.sl
AW247978 2819657.5
AU107934 AU107934
AZ346286 1M0081C01
AU102877 AU102877
                                                                                              March 3, 2003, 22:34:05 ; Search time 2628 Seconds
(vithout alignments)
10753.853 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                           US-10-017-621-3
1745
1 tggaagcagcgtaaaggatg.....gttcacctgcccacttgtcc 1745
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          GenCore version 5.1.4\_p5\_4579 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                       16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                      nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 50
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EST: *

Database

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Result è

Score

45 23.2 21.4 21.2

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human.
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AUTHORS
TITLE
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AW247978
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                                                                                                                                                                                       /doranism="Homo saplens"
/dD_xref='fGDB:3797462"
/dD_xref='fGDB:3797462"
/dD_xref='taxon:9506"
/clone='INAGE:24816'
/clone='INAGE:24816'
/clone='INAGE:24816'
/dev_stage="10 week-post conception fetus"
/dev_stage="20 week-post conception fetus"
/deb_nost-DBH:08 (ampfillin) resistant)"
/dab_nost-DBH:08 (ampfillin) resistant)"
/dab_nost-DBH:08 (ampfillin) resistant)"
/dab_nost-DBH:08 primed for and Spleen: Vector: pT73D (Pharmacia)
/dab_nost-Tranded pDH:08 primed with a pec I - oliqo(dT) primer
/dstanded cDNA was ligated to Eco RI adaptors (Pharmacia), digasted with Pec I and cloned into the Pec I and Eco RI sites of the modified pT773 vector. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington Dilversity School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1810
Fax: 314 286 1810
Email: est@eatson.wustl.edu
Insert Size: 1349
Source: IMAGE Consortium, LLML This clone is available royalty-free
through LLML: contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 1349
Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ### Table 104-MAY-1995

### Add7c08.sl Soares infant brain lNIB Homo sapiens chwa clone IMAGE:25073 3' similar to gb:X66363 SERINE/THREONINE-PROTEIN KINASE PSTARE-1 (HUMAN);, mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(boses 10 28)

M., Hullier, L., Clark, N., Dubeque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rikhi, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Hohldmann, P. and Wilson, R.

Opublished (1995)

Contect: Wilson RR
This clone is available royalty-free through LLNL; contact the ThAGE Consortium (info@image l.lnl.gov) for further information. Trace considered overall poor quality Insert Length: 1418 Std Error: 0.00 Seq primer: reverse ET High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.6%; Score 45; DB 14; Length 46; 97.8%; Pred. No. 0.78; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -21m13
High quality sequence stop: 1.
Location/Qualifiers
1. .28
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Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
R38968/c
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National Institutes of Health, Mammalian Gene Collection (MGC)

I (bases 1 to 48)

National Institutes of Health, Mammalian Gene Collection (MGC)

In (bases 1 to 48)

National Institutes of Health, Mammalian Gene Collection (MGC)

In (bases 2 al9657.3 prime (MGC)

In (bublished (1999)

Onther_ESTS 2 al9657.3 prime (MGC)

Contact: Robert Strausberg, Ph.D.

Email: Gapba-rémail nih, 90v

Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLML) DNA Sequencing by: Berkeley MGC sequencing

project clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLML at:

www-blo.lln.in.gov/DEPprivinage/Ariage.html Base Calling / Quality

Scores: PHRED from University of Washingtion Genome Center

PHRAP suites. Poly T dentification: publach.pl from Berkeley

Drosophila Genome Project. University of Washingtion Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 8 contiguous

PHRED high quality bases following vector sequence. Very Low

Ouality Sequence: Trace file contained 48 contiguous distinct peaks

following vector sequence.
48 bp mRNA linear EST 07-JAN-2000 2819657.5prime NIH_MGC_7 Home sapiens cDNA clone IMAGE:2819657 5', AW247978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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/clone_llb="WIH_WGC_7"
/clsue_type="small cell carcinoma"
/cell_line="WGG3"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.6%; Score 28; DB 14; L
100.0%; Pred. No. 9.1e+03;
tive 0; Mismatches 0;
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High quality sequence stop: 8.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 100.(
Matches 20; Conservative
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/Jab.host-"E. Coll strain XLID-Gold, Tl-resistant, F-
/note-"Vector: PWD42nv; Purified genomic DNA from M.
musculus C578L/6J (male) was obtained from the Jackson
Laboratory Nouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynomically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymuclectide kinase. Adaptor oligomotectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and site-selected for a 9.5 to
10.5 b range using peparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil47321141gblx7129072.1), a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-completent E. coll K110-Gold (Stratagene) cells
and selected for ampleillin resistance.
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
El (Bases 1 to 5)
El (Bases 1 to 5)
El (Bases 1 to 6)
El (Bases 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU102877 Sugano Homo saplens cDNA library Homo saplens cDNA clone COL03075, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 36
/organism-*Mus musculus*
/strain-*C5BL/63*
/db_xref-*taxon:10090*
/clone-*UUGC1M0081CQ1*
/clone-*UUGC1M0081CQ1*
/sex-*Male**
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddune@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0081 row: C column: 01
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 AGATAGGCCTGGATGAGAGTGGTGGTGGTGGCGG 245
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AZ346286.1 GI:10425619
                                                                                                                          house mouse.
Nus musculus
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Eukaryota, Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Butheria; Primates; Catarrhin; Hominidae; Homo.

(bases 1 to 50)
Suzuki, Y. Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H. Ota, T., Isogai, T., Taira, H., Taira, T., Morishita, S., Okubo, K., Sakaki, H., Ota, T., Isogai, T., Tanaka, T., Norishita, S., Okubo, K., Sakaki, Y., Y., Siyama, A. and Sugano, S., Okubo, K., Sakaki, Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

EMBO REP. 2 (5), 386-393 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Emali: ysuzukidims.u-rokyo.ac.jp
Suzuki.Y. Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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/note organ: lung; vector: poTB7; Site_1: XhoI; Site_2: BcoR1; cDNA made by oilgo-dr priming. Directionally cloned into EcoR1/XhoI sites using the following 5 adaptor: GGACGACGAC(G). Size-selected > 500p for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II NT (Life Technologies)."
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/db_xref="taxon:9606"
/clone="HSIO1159"
/note="blffersential display comparison of untreated and dimethyliumarate treated U337 cells"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1573 TCAGGCAGGCCAGCTTTCCGCGTGGTGGACACCGAG 1608
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Gaps

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5009-0-35-HIL.2 Chilcoat/Turkevitz cDNA linear EST 17-JAN-2002 Tetrahymena thermophila cDNA, mRNA sequence.
BN397711 GI:18197764
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2M0279E13F MOUSE 10kb plasmid UUGCZM library Mus musculus genomic
clone UUGCZM0279E13 F, DNA sequence.
AE993993.1 GI:13865220
GSS.
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Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

1 (bases 1 to 50)
Turkeultz, A.P., Karrer, K.M., Jahn, C., Orias, R., Kirk, K.E., Frankel
J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genefics and Cell Biology
University of Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Gaps
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                                                                                                                                                                                                         Query Match 1.2%; Score 21; DB 9; Length 50;
Best Local Similarity 82.8%; Pred. No. 6.3e+05;
Matches 24; Conservative 0; Nismatches 5; Indels
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/strain="CU428.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu
Seq primer: F3.
                                                                                                                                                                                                                                                                                                   558 CAGCCGCCGCCTCCGTCGTCAGCCTAT 586
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                                                                                                                                                                                                                                                                                                                                    Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Department of Virology
Institute of Nedical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukitims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,R., Naruyama,R., Suyama,A. and Sugano
S. Construction and Characterization of a full length-enriched and
a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
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1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,T., Suyama,A. and Sugano,S., Okubo,K., Sakaki,Y., Nakamura,T., Suyama,A. and Sugano,S. Eutelenscriptional initiation revealed by fine, large-scale EMBO Rep. 2 (5), 388-393 (2001)
                                                                                                                                                                                Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Okazu,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Syama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
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Department of Virology
Institute of Wedical Science, University of Tokyo
4-6.1, Shirokanedal, Minaroku, Tokyo 108-8639, Japan
4-6-1, Sulrokanedal, Minaroku, Tokyo 108-8639, Japan
5mail: ysuzukielms.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
Suzuki,Y., Yoshitomo Nakagawa,K., Maruyama, K., Suyama,A. and Sugano
S. Construction and characterization of a full langth-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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                                                                                         Homo sapiens
Bukaryota: Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/clone="CoL03075"
/clone="Libe"Sugano Homo sapiens CDNA library"
/note="Differential display comparison of untreated and dimethyleumarate freated 1937 cells"
a 20 c 10 g feet
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AU105237.1 CI:13554758
  AU102877
AU102877.1 GI:13552398
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/Grow_inlow_wouse luke pissmid oudcin library.
/Grow_inlow_wouse luke pissmid oudcin library.
/Jab_host="E. Coli strain Xil0-Gold, Ti-resistant, F-"
/note="vector: PFD-Zan" | P
                                                           Eukaryota: Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Enkamania: Eutheria: Rodentia; Sciurognathi: Muridae; Murinae; Mus.

1 (bases 1 to 40)
E Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islan, H., Longacres, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly
AM., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
IL Umpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 300, Biomedical Polymers Research Bidg., 20 S. 2030 E., SLC, UT
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AU106960 mRNA sequence.
AU106960 CI: 13556481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="UUGC1M0026F16"
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Fax: 801 585 7177
Fax: 801 585 7177
Fax: 801 585 7177
Insert Length: 10000 5td Error: 0.00
Plate: 0026 row: F column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 48.
Location/Qualifiers
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/strain-"C57BL/6J"
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/drzei-Coybl./61.
/db.zrei-"taxon:10090'
/clone-"uucczy0279213'
/clone-"uucczy0279213'
/clone-"bucczy0279213'
/sax-"Female"
/sax
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/strain="C57BL/61"
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Gaps ö

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil472114)gp[AP12902.1], a copy.number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli KL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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And wight, D., Waiss, R.

House whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

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Rm. 309, Biomedical Polymers
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Dunn, D., Aoyagi, A., Barbar, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                       /sex="Male" //sex="Male" //sex //sex
                                                                                              /strain="C57BL/6J"
/db_ref="text".text".text".clone="UGCJM0059H04"
/clone="UGCJM0059H04"
/clone_lib="Mouse l0kb plasmid UGGIM library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukieins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagava,K., Maruyama,K., Suyama,A. and Sugano
Suzuki,Y., Toshitomo-Nakagava,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
Location/Qualifiers
                               Eukeryota; Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Jiv. Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
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Dunn, D., Aoyagi, A., Barber, M., Boacorn, T., Duval, B., Hamil, C., Islam, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weises, R.
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/organism-"homo sapiens"
/db_xref="taxon:9606"
/clone="cAs09689"
/clone="lb-"sugano Homo sapiens cDNA library"
/note="bifferential display comparison of untreated and
dimethyltumarate treated U937 cells"
a 14 c 18 g 11 t
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: H column: 04
Cidag Pilmer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    922 CTGTTCCAGCTGCTCGTGGCCTGGCCTACTGCCA 956
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Gaps ö

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/(Issue_type='Thymus'
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/(Isb_host='DH)08''
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/(Isb_host='Thymus')
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strousberg, Ph.D.
Email: Gapba: Yamail.nih.gov
Tissue Procurement.nih.gov

Tissue Procurement.nih.gov

Emmert-Buck, M.D., Ph.D.

EDNA Library Preparation: Life Technologias, Inc.

CDNA Library Preparation: Life Technologias, Inc.

CDNA Library Arrayed by: Grag Lannon, Ph.D.

Clone distribution: NGT-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lini.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bono Sapiens
Eukaryota, Netzoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Bono.
1 (bases ito 40)
NOTI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gone Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
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                                                                                                                                                                                                         /db_xref-'taxon:10090*
/clone="INAGE:640424"
/clone=11b='Soares_thymus_2NbWT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trace considered overall poor quality Insert Length: 416 Std Error: 0.00 Seq primer: -40UP from G1bco High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/clone_lib="NCI_CGAP_Colt"
                                                                                                                                   /organism-"Mus musculus"
/strain-"C5781/63"
                        High quality sequence stop: 1. Location/Qualiflers
                                                                                                                                                                                                                                                                                                                            /sex-'male'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
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VERSION
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SOURCE
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DEFINITION
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A1475974/C
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AUTHORS
TITLE
                                                             FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was bydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repeated with 74 DNA polymerase and T4 polymerase dot in the molar excess. The lighted to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (914/2)2114/99/AR129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated vith adaptors complementary to the insert adaptors and adaptored the sheared, adaptored mouse DNA was annealed to chemically-competent E. coil XLIO-Gold (Stratagene) cells and selected for ampicillar resistance.
                                                                                                                                                                                                                                                  /lab_host="E. coll strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PMD4Anv. Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA204601 49-FEB-1997 mRNA linear EST 19-FEB-1997 mu55c05.rl Scares_thymus_2NbwT wus musculus cDNA clone IMAGE:640424 5' similar to SW:1436_BOVIN P29359 14-3-3 PROTEIN GAMMA ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 9)

Marca,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuqua,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Tan,F., Underwood,K., Morris,M., Tan,F., Underwood,K., Moore,B., Materston,R., Materston,R., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-fre. hrough LLNL; contact the IMAGE Consortium (info@image.llnl.go. for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                    /clone_lib-'Mouse 10kb plasmid UGGC2M library'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
Unpublished (1996)
Unpublished (1996)
Unpublished (1996)
Unpublished (1996)
WashU-HHMI Mouse EST Project
WashU-HMIMI Mouse EST Project
WashIngton University School of Medicinep
Washington Ear Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duery Match 1.2%; Score 20.2; DB 17; Length 45; Best Local Similarity 68.3%; Pred. No. 9.5e+05; Matches 28; Conservative 0; Mismatches 13; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28N13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AAGCAGCGTAAAGGATGGACAGGAATGCAGAGGTAGGCAGG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 AAAGAAAAAAAAGGGGGAGAAGGAATGGCGAGGAGGTGG 44
1. .45
/organism="Mus musculus"
/strain="C57BL/63"
/db_kref="taxon:10090"
/clone="UUGC2M0268F01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA204601
AA204601.1 GI:1800608
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    source
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AA204601/c
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KEYWORDS
SOURCE
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us-10-017-621-3.lim50.rst

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/tissue_type-'moderately-differentiated adenocarchoma"
/lab_host-'DH108'
/note-'organ: colon; Vector: pCWV-SPORT6; Site_1: SalI;
Site_2: NOTI: Cloned unidizectionally. Primer: Oligo dT.
Average insert size 1.7 kb. Life Technologies catalog #:
11511-019*
13 c 14 g 4 t
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14 g

ö 0; Gaps Ouery Match 1.1%, Scoro 20; DB 9; Length 40; Best Local Similarity 72.2%; Pred. No. 1e+06; Matches 26; Conservative 0; Mismatches 10; Indels BASE COUNT ORIGIN

Search completed: March 4, 2003, 00:50:32 Job time : 2635 secs . **යු**

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 5', Appl Sequence 75', Appl Sequence 25, Appl Sequence 4', Appl Sequence 11', Appl Sequence 12', Appl Sequence 27', Appl Sequence 27', Appl Sequence 21', Appl Sequence 21', Appl Sequence 21', Appl Sequence 21', Appl Sequence 3', Appl Sequence 21', Appl Sequence 10', Appl Sequence 6', Appl Sequence 6', Appl Sequence 6', Appl Sequence 6', Appl Sequence 6'', Appl Sequence 6'', Appl Description SUMMARTES Query Match Length DB 21:8 21:6 21:4 20:4 20 20

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9 US-09-840-277-107 10 US-09-866-108-15295 9 US-09-938-842-85256 10 US-09-781-5344-18 9 US-10-219-247-31 10 US-09-951-272-31 9 US-09-965-722-31 9 US-09-943-722-31 10 US-09-943-722-31 10 US-09-943-722-31 10 US-09-943-722-31 10 US-09-780-417-233 10 US-09-780-417-233 10 US-09-780-412-4 9 US-10-03-948-14 9 US-10-03-948-14 9 US-10-03-948-25-25 12 US-10-073-256-23 12 US-10-073-256-33 12 US-10-073-256-33 12 US-10-073-256-33 12 US-10-073-256-33 12 US-10-073-256-33 12 US-10-073-256-33 12 US-10-073-256-33 12 US-10-073-256-33 12 US-10-073-256-33	1
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188.6 188.6 188.6 188.2 188.2 188.2 198.2	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

ALIGNMENTS

US-10-054-444-6
Sequence 6, Application US/10054444
Petent No. US/20020164142A1
Sequence 6, Application US/10054444
Fetent No. US/20020164142A1
SENERAL INFORMATION:
APPLICANT: Goldstein, Joel
APPLICANT: Goldstein, Joel
APPLICANT: Bu, Wannen
TITLE OF INVENTION: Recombinant Cat Allergen, Fel dI, Expressed in
APPLICANT: Sun, Wannen
TITLE OF INVENTION: Bacalovirus for Diagnosis and Treatment of Cat Allergy
CURRENT APPLICATION NUMBER: US/10/054,444
CURRENT APPLICATION NUMBER: US/10/054,444
CURRENT FILING DATE: 2002-01-22
PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 6
SOFTHARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 48 Caps ö FEATURE:

1 OTHER INFORMATION: Description of Artificial Sequence:Synthetic US-10-054-44-6 Ouery Match 1.2%; Score 21.8; DB 9; Length 48; Best Local Similarity 70.7%; Pred. No. 9.5e+03; Matches 29; Conservative 0; Mismatches 12; Indels TYPE: DNA ORGANISM: Artificial Sequence

962 AGAAGGTGCTACACCGAGACCTCAAGCCCCAGAACCTGCTC 1002 2 AGAACCICCICCACCAGAACCICCTCCACCAGAACCICCTC 42 Sequence 752, Application US/09801274; Patent No. US20020032319A1 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Cargill, Michale APPLICANT: Ireland, James S. RESULT 2 US-09-801-274-752 ð å

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APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF MRNA
NUMBER OF SEQUENCES: 130
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                 Query Match 1.2%; Score 21; DB 10; Length 31; Best Local Similarity 77.4%; Pred. No. 1.34-04; Matches 24; Conservative 1; Nismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUBER: US 08/050,478
FILING DATE: Z6-CCT-1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUBER: CCT-VS93/02908
FILING DATE: 29-NAR-1993
CLASSIFICATION DATA:
APPLICATION NUBER: US 07/856,747
FILING DATE: 27-NAR-1992
CLASSIFICATION NUBER: US 07/856,747
FILING DATE: 27-NAR-1992
CLASSIFICATION NUBER: 34,398
REGISTRATION NUBER: 34,398
REGISTRATION NUBER: 34,398
TELEPHONE: ADART JOSE-4800
TELEPHONE: (212)758-4800
             PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 94
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                         577 GTCAGCCTATCTGAGATTGGCTTTGGGAAAC 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCCTCCCTGTCAGACMTTGGCTTTGGGAAAC 31
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COMPUTER: IRM PC COMPATIBLE
COMPUTER: IRM PC COMPATIBLE
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ONORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-943-722-47
Sequence 47, Application US/09943722
Publication No. US20020192660A1
GENERAL INFORMATION:
APPLICANT:
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CLASSICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-94
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US-10-029-413A-25
Sequence 25, Application US/10029413A
Sequence 25, Application US/10029413A
Sequence 25, Application US/10029413A
Setting 10 US-1002016535A1
GENERAL INFORMATION:
APPLICANT: Maloud; Timothy C.
TITLE OF INVENTION: Polypeptides and Therapeutic and Screening Methods Using Same
FILE REFERENCE: 421/29
SOURRENT APPLICANTION NUMBER: US/10/029,413A
CURRENT FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 29
SOOFWARE: patentin version 3.1
SEQ 1D NO 25
LENGTH: 45
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APPLICANT: Lander, Eric S.
TILE OF INVERTION: HUMAN SINCLE NUCLECTIDE POLYMORPHISMS
FILE REFERENCE: 2825, 2009.001
CURRENT APPLICATION NUMBER: US/09/801.274
CURRENT APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000.03.07
PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000.05.22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FastSEQ for Windows Version 4.0
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; Patent No. US/2002032319A1
; Patent No. US/2002032319A1
; Patent No. US/2002032319A1
; APPLICANT: Cargill, Michala
; APPLICANT: Ireland, James S.
; APPLICANT: Ireland, James S.
; TITLE OF INVERTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; TITLE OF INVERTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR PLICATION NUMBER: US/60/187,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      907 AACGIGAAACIGIICCIGIICCAGCIGCICC 937
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US-09-801-274-752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: partial_cDNA; LOCATION: (1)..(45); OTHER INFORMATION: US-10-029-413A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-601-274-94
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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RESULT 9
US-09-790-417-235/c
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HUDSON, Peter John
APPLICANT: HUDSON, Peter John
APPLICANT: HUDSON, Peter John
APPLICANT: ROBERT, Alex Andrew
APPLICANT: ATRELGATON LA ALEXANDER
TITLE OF INVENTION: HIGH AVIDITY POLYVALENT AND POLISPECIFIC REAGENTS
FILE REPERRECE: 016786/0212
CURRENT APPLICATION NUMBER: US/09/147,142
CURRENT FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: PCT/AU38/00212
BARLIER FILING DATE: 1998-03-27
SARLIER FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PALENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HUDSON, PETCH John
APPLICANT: HUDSON, PETCH John
APPLICANT: HUDSON, PETCH JOHN
APPLICANT: KORTT, Alex Andrew
APPLICANT: KORTT, Alex Andrew
APPLICANT: ATWING, Robert Alexander
APPLICANT: ATWELL, John Lealie
TITLE CO INVERTION: HICH AVIDITY POLTVALENT AND POLYSPECIFIC REAGENTS
FILE REFERENCE: 016796/0212
CURRENT FILIGE DATE: 1999-03-05
EARLIER FILING DATE: 1999-03-05
EARLIER FILING DATE: 1999-03-05
EARLIER FILING DATE: 1999-03-05
MUMBER OF SEQ ID NOS: 32
NUMBER OF SEQ ID NOS: 32
                                                                                                                               Gaps
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OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: oligonuclectide used to insert codon between VH
OTHER INFORMATION: and VL domains of NCIO scFv-0
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                                                                              Length 48;
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                                                                   Query Match 1.2%; Score 20.4; DB 9; Length 4 Best Local Similarity 71.1%; Prad. No. 2.3a+04; Matches 27; Conservative 0; Mismatches 11; Indals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          643 GGTACCTATGCCACCGTCTACAAAGGCAAAAGCAAGGTCACAGA 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGACCACGGTCACCGTCTCCGGTGGTGATATCGAGCTCACACA 44
                                                                                                                                                             325 GAGATTGTGCACGAGGACTTGAAGATGGGGTCTGATGG 362
                                                                                                                                                                                          1111 | 111 | 1 | 1 | 1111| | 111 | 1111| 7 GAGACGGAGGATGGATGG 44
                                                                                                                                                                                                                                                                                                                                    : Sequence 11, Application US/09147142
: Patent No. US20020018749A1
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/09147142; Patent No. US20020018749A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
  LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-147-142-12/c
; TOPOLOGY;
US-09-943-722-47
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LENGTH: 45
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GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Roop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: oligonucleotide used to insert codon between VH
OTHER INFORMATION: and VL domains of NCIO serv-0
US-09-147-142-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                Length 45;
                                                                                                                                        Query Watch 1.1%; Score 20; DB 10; Length 45
Best Local Similarity 65.9%; Pred. No. 2.8e+04;
Matches 29; Conservative 0; Nismatches 15; Indels
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                                                                                                                                                                                                                                 643 GGTACCTATGCCACCGTCTACAAAGGCAAAAGCAAGCTCACAGA 686
                                                                                                                                                                                                                                                             3, DB 10; 3c+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REDABLE FORM:
WEDLUM TYPE: Floppy disk
WEDLUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTMARE: PECHOTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
CILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MCHASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECONMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 758:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.1%; Score 19.8; C
Best Local Similarity 77.4%; Pred. No. 3c+0
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1689 CTTCCCTGCTTACTCTCTGCCTACCTGCCTG 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CTTCCTTCTTTCTTCTTCTGCCTGCCTG 33
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 758, Application US/09263959
Patent No. US20020150891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 235, Application US/09790417
Patent No. US20010031470A1
GRMEAL INPORMATION:
APPLICANT: Shult, John W
APPLICANT: Lewis, Martin K.
APPLICANT: Lieppe, Donna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
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ZIP: 98104-7092
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RESULT 12
US-09-801-274-517
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US-10-073-256-27/C
US-10-073-256-27/C
Sequence 27, Application US/10073256
Factor No. US20020120408A1
Factor No. US20020120408A1
Factor No. US20020120408A1
FAPPLICANT: Kreiswirth, Barry N
TITLE OF INVERTION:
FILE REFERENCE: 19124-0007
FILE REFERENCE: 19124-0007
FILE REFERENCE: 2002-02-13
KUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
FILE NOW NOTE OF SEQ ID NOS: 80
FILE NOW NOTE OF SEQ ID NOS: 80
FILE NOS: 80
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Patent No. US20020120408A1
CENERAL INFORMATION.
CENERAL THORMATION.
APPLICANT: Kreiswirth, Barry N
APPLICANT: Radich, Steven M
TILE OF INVENTION: System and Method for Tracking and Controlling Infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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US-09-790-417-235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 1.14; Score 19.4; DB 7; Length 45; Best Local Similarity 64.44; Pred. No. 4.1e+. Matches 29; Conservative 0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 GTACCTGGTAAATGAACTCACCCACGATATCATCACCAAGCT 1
APPLICANT: Mandrekar, Michelle
APPLICANT: Rephart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Marchet, James R.
APPLICANT: Olson, Ryan J.
APPLICANT: Olson, Ryan J.
APPLICANT: Weach, Roy
TITLE OF INVENTION: NUCLEIC Acid Detection
FILE REFERENCE: Pro-103 6868/7528
CURRENT APPLICATION NUMBER: 05/958972
PRIOR PELICATION NUMBER: 09/958972
PRIOR PELICATION NUMBER: 09/958973
PRIOR PELICATION NUMBER: 09/9587
PRIOR PELICATION NUMBER: 09/9581
NUMBER OF SEQ ID NOS: 290
SEQ ID NO 215
FENCINAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-073-256-27
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OKGANISM: Artificial Sequence
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US-10-073-256-35/c
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US-09-263-959-121/C
Sequence 121, Application US/09263959
Percent No. US20020150891A1
GENERAL INFORMATION:
APPLICANT: ROWEN, Lee
APPLICANT: ROWEN, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND WETHODS WHICH UNAURER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Retent No. US20020012319A1

GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Ireland, James S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2852.2009-001
CURRENT APPLICATION HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2001-03-07
CURRENT APPLICATION NUMBER: US 60/187, S10
FRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
SPRIOR FILING DATE: 2000-03-07
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STREET: 6300 Columbia Center, 701 Fifth Avenue
FILE REFERENCE: 19124.0002
CURRENT APPLICATION NUMBER: US/10/073,256
CURRENT FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1190 CCACAGGCCGTCCCTCTTTCCGGGC 1215
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CITY: Seatile
STATE: Heahington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-073-256-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
US-09-801-274-517
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1343 CCCTTTTGAGCCACGCACCCGACTTGATAGCGAC 1377
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Publication No. US20020192813A1

SEMERAL INFORMATION

APPLICANT: Conner, Timothy W

APPLICANT: Sontino, Colleen G

ITLE OF INVENTION: No. US20020192813A1e1 Plant Expression Vectors

FILE REFERENCE: monocot elementa

CURRENT APPLICATION NUMBER: US/09/376,940A

CURRENT APPLICATION NUMBER: 60/097150

EARLIER APPLICATION NUMBER: 60/097150

SAFRIER PLING DATE: 1998-08-19

NUMBER OF SED ID NOS: 63

SEOFWARE: Patentin Ver. 2.1

LENGTH: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.14; Score 19.2; DB 10; Length 46; 75.0%; Pred, No. 4.7e+04; tive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.14; Score 19; DB 9; Length 43; Best Local Similarity 65.14; Pred. No. 5.1e+04; Matches 28; Conservative 0; Mismatches 15; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
CLASSIFICATION:
NAME: MCMASTERS, DAVID D.
REGISTRATION NUMBER: 33,963
REFRENCE/DOCKET NUMBER: 92010.426C2
FELECOMMUNICATION INFORMATION:
FELECOMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/09818066
Patont No. US20020032307A1
GENERAL INFORMATION:
APPLICANT: Shuping Tong et al.
TITLE OF INVENTION: HEPADNAVIRUS RECEPTOR
NUMBER OF SEQUENCE: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flah & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 GCACCAGAGATTGTGCACGAGGACTTGAAGAT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 GCACCAGAGTTTCTGCACAGGGAGGGGGAGAT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0uery Match 1.14
Best Local Similarity 75.04
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-376-940-23/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
US-09-263-959-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-818-066-32
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Caps
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                            COMPUTE: U.S.A.

COMPUTE: 0.110-2804

COMPUTER: U.S.A.

COMPUTER: TADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTES: IBM PC compatible

OPERATING SYSTEM: F0-DS/MS-DS.

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/#18,066

FILING DATE: 2-War-2001

CLASSIPICATION CUNROWN>

PRIOR APPLICATION NUMBER: US 08/683,262

FILING DATE: 18-JUL-1996

ATTORNEY/AGNT INFORMATION:

NAME: Fraser, Janis K.

RESISTRATION NUMBER: 31.819

REFERENCE/DOCKET NUMBER: 00786/287002

FELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
1.1%; Score 19; DB 10; Length 45;
Best Local Similarity 71.4%; Pred. No. 5.2e+04;
Matches 25; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear seq ID NO: 32: US-09-818-066-32
STATE: Massachusetts
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2 CCCTTTTGAGCCACGAATTCCAGGATGAAACAGAC 36

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Search completed: March 4, 2003, 00:54:25 Job time : 134 secs

\$82, App \$82, App \$82, App \$82, App \$82, App \$82, App \$83, App \$84, App \$85, App \$85

Sequence Seq

Scoring table: Perfect score:

Searched:

Seguence:

Run on:

Database :

```
RESULT 1
US-08-334-177-5
1 Sequence 5, Application US/08334177
1 Sequence 5, Application US/08334177
2 Patent No. 5696086
2 GENERAL INFORMATION:
3 APPLICANT: Arraham, Hava Karsenty
3 APPLICANT: Godowski, Paul J.
3 APPLICANT: Godowski, Paul J.
4 APPLICANT: Godowski, Paul J.
5 TITLE OF INVENTION: Methods and Kits Using Macrophage Stimulating Protein
6 CONRESPONDENCES:
7 CONRESPONDENCES:
7 CONRESPONDENCE:
7 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Local Similarity 69.8%; Pred. No. 5.8e+03;
nes 30; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Generach, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ILP: 94080
COMPUTER READABLE FORM:
WEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/34,177
FILING DATE:
    US-08-078-683A-27
US-08-206-176-19
US-08-1171-189-582
US-08-121-936-582
US-08-475-228A-582
US-08-475-228A-582
US-08-475-218-582
US-09-375-118-11
US-08-752-644-38
US-08-752-644-38
US-08-752-18-5
PCT-US93-106-38
US-08-752-18-5
US-08-732-18-5
US-08-732-18-5
US-08-732-18-5
US-08-732-18-5
US-08-732-18-5
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REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 912
TELECONOMULCATION INFORMATION:
TELEFRAX: 415,725-5416
TELEFRAX: 415,952-981
TELEX: 910,731-716
INFORMATION FOR SED ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
STOPOLOGY: linear
US-08-334-177-5
119.6
119.6
119.6
119.2
119.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
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Sequence 5, Appli
Sequence 9, Appli
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                                                                                                                                                                                                                                                   March 3, 2003, 22:35:55 ; Search time 76 Seconds (without alignments) 7041.460 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 tggaagcagcgtaaaggatg.....gttcacctgcccacttgtcc 1745
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                      GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-507-4262-9
US-08-171-189-156
US-08-171-189-156
US-08-475-228A-156
US-08-482-080A-156
US-09-34-447-156
PCT-US33-17388-156
US-08-233-009-33
US-08-487-860-38
US-08-850-049-47
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US-09-414-117-47
US-09-444-700-21
US-09-150-848-13
US-09-150-864A-13
US-08-52-186-33
US-08-531-186-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 04
Maximum Match 1004
Listing first 45 summaries
                                                                                                                                                                              nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-017-621-3
1745
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Match Length D
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Gaps

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PCT-US95-13830-5

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Gaps
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     FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:Synthetic

OTHER INFORMATION: ribozymes and portions thereof
US-08-507-426C-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Edwards, Cynthla A. APPLICANT: Cantor, Charles R. APPLICANT: Cantor, Charles R. APPLICANT: Turin, Lisa M. APPLICANT: Turin, Lisa M. APPLICANT: Fry, Kirk E. TITLE OF INVERTION: Sequence-Directed DNA Binding TITLE OF INVERTION: Noiecules, Compositions and Methods NUMBER OF SEQUENCES: ADDRESSE: Genelabs Technologies, Inc. STREET: 505 Penobscot Drive CITY: Redwood City
                                                                                                                             Ouery Match 1.2%; Score 21.8; DB 4; Length 44;
Best Local Similarity 70.7%; Pred. No. 7.2e+03;
Matches 29; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                            Qy 1559 CGTCGATGCCTGACTCAGGCGAGGCTTTCCGCGTGGTG 1599
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HOLDCULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORGINAL SOURCE:
INDIVIDUAL ISOLATE: Human H1 histone gene FNC16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94063

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pattentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
                                                                                                                                                                                                                                                          4600-0175/G19P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PELGATION TO ATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REFERENCE/DOCKET NUMBER: 4600-0175/631
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 156, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 374-0960
INPORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-08-171-389-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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US-08-507-426C-9/C

US-08-507-426C-9/C

Sequence 9, Application US/08507426C.

Sequence 9, Application US/08507426C.

Sequence 9, Application US/08507426C.

Sequence 9, Application US/08507426C.

Sequence 9, Application William Companies of Conferring On Plants Resistance of Invertion Polyremozyne Tille OF Invertion: POLYREBOZYNE TILLE OF INVERTION: POLYREBOZYNE FILLE REFERBNCE: 43944-A-PCT-US

CORRENT FILING DATE: 1995-10-25

PRIOR FILING DATE: 1995-10-25

WUMBER OF SEQ ID NOS: 14

SEQ ID NOS: 14

SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                              APPLICANT: Geneticch, Inc.
APPLICANT: Rew England Deaconess Hospital Corp.
TITLE OF INVENTION: Methods and Kits Using Nacrophage Stimulating
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genericch, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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2 GGACGAATCCACCATGGGGTGGCTCCCACTCCTGCTGCTTCTG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUW TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTHARE: Winbatin (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GGCGGCAGTGACCCTGGAGGCCCCCCACACGTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0912PCT
TELEPHONE: 415/225-516
TELEPHONE: 415/952-9881
                                                                                                                       : Sequence 5, Application PC/TUS9513830
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415/952-9881
TELEX: 910/3717-7166
INFORMATION FOR SEG ID NO: 5: SEGUENCE CHARACTERISTICS: LENGTH: 47 Dase pairs TYPE: Nucleic Acid STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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; TOPOLOGY: PCT-US95-13830-5

Matches

ò g

ò a Edwards, Cynthia A.

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Gaps ö

Indels

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Query Match 1.2%; Score 21.4; DB 2; Length 46; Best Local Similarity 71.8%; Pred. No. 9.3e+03; Matches 28; Conservative 0; Mismatches 11; Indels
                                                                  GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Fry, Kirk E.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06-JUN-1955
PRIOR APPLICATION NUMBER: 05-JUN-1955
PRIOR APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA: US 08/081,070
FILING DATE: 27-JUN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 27-JUN-1993
APPLICATION NUMBER: US 08/081,070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE: Human H1 histone gene FNC16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATE: US/08/475,228A FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1641 GCGGCTGGAGGGATGCCACACCCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GCGGTGGATTGGACGCTCCACTAATCACAGGGCAGCGCC 40
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genelabs Technologies, Inc. STREET: 505 Penobscot Drive CITY: Redwood City
                    ; Sequence 156, Application US/08475228A
; Patent No. 5869241
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94063
COMPUTER REALABLE FORM:
WEDJUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
105-08-482-080A-156
1 Sequence 155, Application US/08482080A
1 Fatent No. 6010849
1 GENERAL INPERATION:
1 APPLICANT: Edwards, Cynthia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAONE: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double
                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; INDIVIDUAL 1
US-08-475-228A-156
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                     Gaps
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                                                                                                                                                                                                                                                                                 Sequence 156, Application US/08123936

Patent No. 5726014

GERERAL INFORMATION:
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
TILLE OF INVENTION: Screening Assay for the Detection of TILLE OF INVENTION: DNA-Binding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCES: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
CART.
Ouery Match 1.2%; Score 21.4; DB 1; Length 46; Best Local Similarity 71.8%; Fred. No. 9.3e+03; Matches 28; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.2%; Score 21.4; DB 1; Length 46; 71.8%; Pred. No. 9.37.403; tive 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
                                                                                                   1641 GCGGCTGGAGGGATGCCACACCCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; INDIVIDUAL ISOLATE: Human H1 histone gene FNC16
US-08-123-936-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1641 GCGGCTGGAGGGATGCCACACCCCTCACAGGGCAGCCCC 1679
                                                                                                                                     2 GCGGTGGATTGGACGTCCACCATCACAGGGCAGCGCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GCGTGGATTGGACGCTCCACCAATCACAGGCCAGCGCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4600-0075.32/G19P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fablan, GGTY R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOOKET NUMBER: 4600-
TELECOMUNICATION INFORMER: 4600-
TELEFAC: (415) 324-0860
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENTTH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11near
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
1.2%
Best Local Similarity 71.8%
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                08-123-936-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ReSTATE: COUNTRY:
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Query Match 1.2%; Score 21.4; DB 4; Length 46; Best Local Similarity 71.8%; Pred. No. 9.3e+03; Matches 28; Conservative 0; Mismatches 11; Indels
           APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TILLE OF INVENTION: Sequence-Directed DNA Binding
TILLE OF INVENTION: Molecules, Compositions and Nethods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSES: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-Directed DNA Binding
Molecules, Compositions and Methods
641
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TIPE: Floppy disk
MEDIUM TIPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/09/354,947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human H1 histone gene PNC16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OY 1641 GCGCTGGAGGGATGCCACACCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMUNICATION INFORMATION:
TELEFAN (650) 324-0880
TELEFAN: (650) 324-0860
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GCGGTGGATTGGACGCTCCACCAATCACAGGCAGCGCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/482,080
FILING DATE: 07-JUN-1993
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
APPLICATION NUMBER: US 07/723,618
FILING DATE: 23-DEC-1992
APPLICATION NUMBER: US 07/723,618
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 22-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 22-JUN-1991
AND APPLICATION NUMBER: US 07/723,618
FILING DATE: 22-JUN-1991
AUDICATION NUMBER: US 07/723,618
FILING DATE: 22-JUN-1991
AUDICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 156, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Sequence-Directe
TITLE OF INVENTION: Molecules, Compo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
NOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: double
                                                                                                                                                                                                                                       Redwood City
                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US93-12388-156
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                                                                                                                                                                                                                                                           STATE: C.
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APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Andrews, Beth M.
APPLICANT: Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
TITLE OF INVENTION: Molecules, Compositions and Methods
TORRESPONDENCE ADDRESS: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STRY: Redwood City
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 1.2%; Score 21.4; DB 3; Length 46; Best Local Similarity 71.8%; Pred. No. 9.38+03; Matches 28; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 20-DEC-1993
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : INDIVIDUAL ISOLATE: Human H1 histone gene FNC16 US-08-482-080A-156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
FEFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GCGGTGGATTGGACGCTCCACCAATCACAGGGCAGCGCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION WUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PHOR APPLICATION DATA:
APPLICATION WUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
RIOR APPLICATION UNMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 156, Application US/09354947
Patent No. 6384208
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (650) 324-080
TELEFAX: (650) 324-080
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGIAAL SOURCE:
                                                                                                                                                                                                                                                                                                                                              ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-09-354-947-156
                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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APPLICANT: Tellon, Dale
APPLICANT: Glaser, Scott
APPLICANT: Glaser, Scott
APPLICANT: Hose, Walliam
APPLICANT: Hose, Walliam
TITLE OF INVENTION: No. 5728821el Mutant BR96 Antibodies and
TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas
CORRESPONDENCE, ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.2%; Score 20.6; DB 1; Length 45; Best Local Similarity 67.4%; Pred. No. 1.5e+04; Matches 29; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      737 CCTGCACCGCCATCCGGGAAGTGTCCCTGCTCAAGGACCTCAA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 90035-3335
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NDATA:
RPLICATION NUMBER: US/08/285,936
FILING DATE: 04-AUG-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Bldv., Suite 400
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REPERENCE/DOCKET NUMBER: 30436.16US01
RELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
TTPE: nucleic acid
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,009
FILING DATE: 25-APR-1994
CLEASTEICATION: 424
ATTORNEY/ACENT INPORMATION: 424
ATTORNEY/ACENT INPORMATION: 424
ATTORNEY/ACENT INPORMATION: 19219
TELECOMMUNICATION NUMBER: 19219
TELEPHONE: 1908) 594-3901
TELEPHONE: (908) 594-3901
TELEPHONE: 1908) 594-3701
SEDUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-08-285-916-38/C
Sequence 38, Application US/08285936
Patent No. 5728821
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDENESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE:
US-08-233-009-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
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Patent No. 5646156
GENERAL INFORMATION:
APPLICANT: Jacobson, Marlene A
APPLICANT: Jacobson, Robert G
APPLICANT: Salvacore, Christopher A
TITLE OF INVENTION: ACTIVATION THROUGH A3 ADENOSINE RECEPTOR ANTAGONISM
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: D. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
1.2%; Score 21.4; DB 5; Length 46;
Best Local Similarity 71.8%; Pred. No. 9.3e+03;
Matches 28; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 27-DEC-1992
FILING DATE: 27-DEC-1992
ATTORN WINBER: 33,875
RECERRICATION NUMBER: 33,875
RECERRICATION NUMBER: 43,875
RECERRICATION NUMBER: 460-0175.41/G19PCT2
FELECONNUNICATION INFORMATION:
TELECONNUNICATION INFORMATION:
FELERAM: (415) 324-0860
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: LINEAR
HOPOLOGY: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INTIVIDUAL ISOLATE: Human H1 histone gene FNC16
PCT-US93-12388-156
                                                                                                                                                                                                        MEDINATYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07065
COMPUTER REMDABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OY 1641 GCGCTGGAGGATGCCACACCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GCGGTGGATTGGACGCTCCACCAATCACAGGGCAGCGCC 40
               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Rahway
STATE: New Jersey
COUNTRY: United States
ZIP: 07065
                                                                                                                                                                              COMPUTER READABLE FORM:
                                                          STREET: 505 Pences.
CITY: Redwood City
                                                                                                                                                           94063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-233-009-33
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Gaps ö

us-10-017-621-3.lim50.rni

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        TILLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF MRNA NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: WORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INMIBITORY/INSTABILITY REGIONS OF MRNA
NUMBER OF SECONDENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.2%; Score 20.4; DB 2; Length 48; Best Local Similarity 71.1%; Pred. No. 1.7e+04; Matches 27; Conservative 0; Mismatches 11; Indels
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SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION NATA:
PPLICATION NATA:
PPLICATION WINDER: US/08/650.049
FILING DATE: U2-MAY-1997
CLASSIFICATION NATA:
APPLICATION NATA:
APPLICATION NAMER: US 08/050.478
FILING DATE: 26-OCT-1994
CLASSIFICATION NAMER: QS-OCT-1994
CLASSIFICATION NAMER: QS-OCT-1994
FILING DATE: 29-WAR-1993
CLASSIFICATION NAMER: QS-OCT-1994
FILING DATE: 27-WAR-1993
CLASSIFICATION NAMER: WS 07/658.747
FILING DATE: 27-WAR-1992
CLASSIFICATION NAMER: US 07/658.747
FILING DATE: 27-WAR-1992
CLASSIFICATION NAMER: 34,396
FILING DATE: 27-WAR-1992
CLASSIFICATION NAMER: 2056-4006US1
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
INFORMATION NAMER: 2026-4006
TELEFAX: (212)751-6849
INFORMATION POR SED ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: AB BASE PAIRS
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-08-050-478-47
Sequence 47, Application US/08050478
Patent No. 5972596
GENERAL INFORMATION:
APPLICANT:
APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING STSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: SI
TOPOLOGY: LINEAR
US-08-850-049-47
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STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                        US-06-487-860-38/c
US-06-487-860-38/c
Patent No. 5792456
GENERAL INFORMATION:
APPLICANT: Velton, Dale
APPLICANT: Glaser, Scott
APPLICANT: Rosok, Mae J.
TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas
NUMBER OF SEQUENCES: 62
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                                                                    Query Match 1.24; Score 20.6; DB 1; Length 45; Best Local Similarity 67.44; Pred. No. 1.5e+04; Natches 29; Conservative 0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYRE: Floppy disk
COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PACENTIN Release #1.0, Version #1.25
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/487,860
FILING DATA:
OTHER DATE: 07-JUN-195
CLASSIFICATION SOR #1.05
ATTORNEY/AGBUT INFORMATION:
NAME: Adriano, Sarah B.
REGISTERNCE/DOCKET NUMBER: 34.470
REFERENCE/DOCKET NUMBER: 34.470
REFERENCE/DOCKET NUMBER: 34.470
REFERENCE/DOCKET NUMBER: 34.450
TELECOMUNICATION THYOMATION:
TELECOMUNICATION THYOMATION:
TELEFRAM: 310-445-41140
TELEFRAM: 310-445-4011
INFORMATION FOR SEO ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: single
                                                                                                                                                                                                                  328 ATTGTGCACGAGGACTTGAAGATGGGGTCTGATGGGGAGAGTG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 ATTGTGCACGAGGACTTGAAGATGGGGTCTGATGGGGAGAGTG 370
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Bldv., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-850-049-47
Sequence 47, Application US/08850049
Patent No. 5965736
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: LOS
STATE: CA
COUNTRY: U
05-08-285-936-38
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
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õ 8 29-MAR-1993

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325 GAGATTGTGCACGAGGACTTGAAGATGGGGTCTGATGG 362
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                                                                                                                            CLASSIFICATION

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/858,747

FILING DATE: 27-MAR-1992

CLASSIFICATION:
ATTONEY FACENT TWORM-TION:
NAME: MORRY, MARY J.

REGISTRATION NUMBER: 34,398

REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2026-4006US1

FLEEPHONE: (212)751-649

INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 BASE PAIRS

TPPE: NUCLEIC ACID

STRANDENSS: SINGLE

US-09-414-117-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: March 4, 2003, 00:52:00 Job time : 80 secs
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Best Local Similarity 71.10
Matches 27; Conservative
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Sequence 47, Application US/09414117

Patent No. 6291664

GERERAL INFORMATION:

APPLICANT:
ANDI:
APPLICANT:
APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 1.2%; Score 20.4; DB 2; Length 48; Best Local Similarity 71.1%; Pred. No. 1.7e+04; Matches 27; Conscrvative 0; Mismatches 11; Indels
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,478
FLING DATE: 26-CCT-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION WINBER: PCT/US93/02908
FILING DATE: 27-MAR-1992
CLASSIFICATION WINBER: US/07/058/747
FILING DATE: 27-MAR-1992
CLASSIFICATION: A35
ATTORNEY AGENT INFORMATION:
NAME: WORRY J. MARY J.
REGISTATION NUMBER: 2026-4006USI
FLEEDANE: (212)751-6849
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINCLE
TOPOLOGY: LINRAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325 GAGATTGTGCACGAGGACTTGAAGATGGGGTCTGATGG 362
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/US93/02908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-414-117-47
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Gaps ö

1.2%; Score 20.4; DB 4; Length 48; 71.1%; Pred. No. 1.7e+04; ttive 0; Mismatches 11; Indels

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March 3, 2003, 19:29:35 ; Search time 427 Seconds
(without alignments)
9203.131 Million cell updates/sec
                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                       US-10-017-621-3
1745
1 tggaagcagcataaaggatg.....gttcacctgcccacttgtcc 1745
   GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                         Total number of hits satisfying chosen parameters:
                                                                   2185239 seqs, 1125999159 residues
                                                                                             Post-processing: Minimum Match 0N
Maximum Match 100%
Listing first 45 summaries
                 nucleic search, using sw model
                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                  Minimum DB seq length: 0 Maximum DB seq length: 50
                                                                                                                             Title:
Perfect score:
                                                        Scoring table:
                 OM nucleic -
                                                Sequence:
                                                                   Searched:
                                                                                                             Database
                         Run on:
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Description	Human SNP oligonuc Human Cdk5 related Human Cdk5 related Human angle nucle Human silent SNP c PK priner SRS fo ifnG coding region Human Hl histone g
SUMMARIES	AAL3435 ABA0409 ABA04100 AAI30364 AAI75839 AAI25606 AAH2253 AAD29563
80	22222222
% Query Match Length DB ID	
Query Match	40000000000
Score	22 22 23 24 4 4 4 4 4 4 4 4 4 4 4 4 4 4
ult Ro.	
Result No.	ບບ ບບ

Human Hl histone grest sequence from DNA binding molecu PCTAIRE-1 polymorp Human cervical can Human SNP oligonuc DE1971651 primer FT-PCR primer for hum Human SNP oligonuc Xcdsi degenerate p HIV pol INS mutage PCR primer for amplify Human 4-1BB 3' PCR Human 4-1BB 3' PCR Human cytokine rec	Human prostate spe MOSIGHAEI House Ig Rectse CFC primer Corneodesmosin ain CD1+ human T-lymph Human large protei IL-6R and IL-6 fus Human SNP oligonuc Human SNP oligonuc Human SNP oligonuc Human ADb adenosin Human ADb adenosin Human adenosine AD Low adenosine AD Human adenosine AD Low adenosine AD Low adenosine AD Human aldenosine AD Human aldenosine AD	3.35/c 3.45/3.35 standard; DNA; 50 BP. AAL34335; AAL34335; 24-JAN-2002 (first entry) Human SNP oligonucleotide #7543. Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; anylase; cencer; amylof protein; angiopotetin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony studiating factor; complement related protein; cytochrome; kinasin; cytokine; interferor; interferorial interleukin; Grobin couplad receptor; thloesterase; inflammation; nervous system disease; aucimmune disease; infection; Homo sapiens. 40200147944-A2. 28-DEC-1099; 99US-0173419; 27-DEC-2000; 2000US-0173419; 27-DEC-2000; 2000US-0173419;
AAT63868 AAX17156 AAK16267 AAH62195 AAK134286 AAX134286 AAX10679 AAT00670 AAT00670 AAT00670 AAT00670 AAT00670 AAT00670 AAT00670 AAT00670	ANEK 6870 AND 1379 ANE 1379 ANE 31379 ANE 31379 ANE 31379 ANE 31379 ANE 3138 ANE 313	P. Mulatory; antiani; gene there in; apoptosis in histone; kircytochrome; kied receptor; kied receptor; timmune disease
22222222222222222222222222222222222222	22222222222222222222222222222222222222	50 Bi yy
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4440N4444NN44444	(first entry) (first entry) igonucleotide ssive; immunos ive; antimicro ein; angiopoie entra; oncoge elated protein G protein cou d disease; ss em disease; ss 2000WO-US3549 99US-017341 2000US-017341
		standard; i); i002 (first r oligonucl rpotesh; an protein; an protein; an protein; an related int related int related trin; G-prote trin; G-prot
122 200 200 200 200 200 200 200 200 200	70007 700007 700007 700007 70007 70007 70007 70007 70007 70007 70007 70007 700	T. 1 3.35/c AAL34335 st. AAL34335; 24-JAN-2002 Human SNP o Immunosuppr neuroprotec amyloid pro complement interlaukin multifactor nervous sysi Homo saplem 40200147944 05-JUL-2001 28-DEC-1999, 27-DEC-2000, 28-DEC-1999,
110 111 113 113 114 116 117 118 118 118 127 127 128 128 128 129 129 120 120 120 120 120 120 120 120 120 120	786000000000000000000000000000000000000	AAL35/AAL35/AAL35/AAL35/AAL35/AAL35/AAL35/AAL36/
000 00 0	U U U	A MESULE A M

Gaps

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Length 33; Indels

1.3%; Score 22.4; DB 24; B1.2%; Pred. No. 2.8e+04; tive 0; Mismatches 6;

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The present invention describes medicinal compositions (I) inhibiting beta-amyloid production comprising an active component a substance that inhibits the activity of eyclin-dependent kinase (CDK). Also described are: (I) a method for screening compounds for their ability to inhibit the production of beta-amyloid by contacting with beta-amyloid producing cells; and (2) screening kits. (I) have mootropic and neuroprotective activities. (I) suppress the phosphorylation of amyloid precursor protein (APP) which is an essential step in the production of beta-amyloid. (I) such as demonstrated and prevention of neurodependentive diseases such as demonstrate disease. The prosent sequence represents a pRR primer which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                    Sequence 33 BP; 6 A; 6 C; 11 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1018 GAGCTCAAGCTGGCTGACTTTGGCCTGGCCCG 1049
                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 81.20
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
            8
                                                                                                                                                                                                                     The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoletin, cappoposis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, comproteins, cytochromes, kinesins, cytokines, interferons, interleukins, component coupled receptors and thioesterases. The present sequence is one such oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of disasses associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include cisasses (e.g. rheumatoid arthitis, multiple sclerosis, diabetes) consulting expension to the padder, brain, breast, colon and kidney, chemical diseases of the nervous system and an infection of pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                         Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicinal compositions for the treatment of dementia and Alzheimer's disease, comprise compounds that suppress beta amyloid production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; beta-amylold; cyclin-dependent kinase inhibitor; nerve cell;
amylold precursor protein; APP; Cdk5; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.4%; Score 24.8; DB 22; 72.7%; Pred. No. 7.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50 BP; 7 A; 13 C; 14 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hachlya S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Cdk5 related PCR primer SEQ ID NO:18.
                                                                                                                                                                                       Claim 1; Page 3563; 4143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suzuki T, Watanabe T, Kawabata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 23; 62pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (YAMA ) YAMANOUCHI PHARM CO LTD. (SUZU/) SUZUKI T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA04099 standard; DNA; 33 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-APR-2001; 2001WO-JP03555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-APR-2000; 2000JP-0131037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
     Leach M;
                                             WPI; 2001-465210/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4PI; 2002-026209/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W0200182967-A1.
Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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The present invention describes medicinal compositions (1) inhibiting beta-amyloid production comprising an active component a substance that inhibits the activity of cyclin-dependent kinase (CBK). Also described are: (1) a method for screening campounds for thair ability to inhibit the production of beta-amyloid by contacting with beta-amyloid producing cells; and (2) screening kits. (1) have mostropic and neuroprofective activities. (1) suppress the phosphorylation of amyloid precursor protein (ARP) which is an essential step in the production of beta-amyloid. (1) such as dementia and Alzheimer's disease. The present sequence represents a PCR primer which is used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicinal compositions for the treatment of dementia and Alzheimer's disease, comprise compounds that suppress beta amyloid production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; beta-amyloid; cyclin-dependent kinase inhibitor; nerve cell; amyloid precursor protein; APP; Cdk5; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hachiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Cdk5 related PCR primer SEQ ID NO:19.
2 GAGCTGAAATTGGCTAATTTTGGCCTGGCTCG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawabata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 23; 62pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (YAMA ) YAMANOUCHI PHARM CO LTD. (SUZU/) SUZUKI T.
                                                                                                                                                                                                                                        HP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-2000; 2000JP-0131037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-APR-2001; 2001WO-JP03555.
                                                                                                                                            RESULT 3
ABA04100/c
ID ABA04100 standard; DNA; 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-026209/03.
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(first entry)

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Human; single nucleotide polymorphism; SNP; genome; gene therapy; protein therapy; vaccine; probe; diagnostic assay; detection; quantitation; restorative therapy; polymorphic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic nucleic acid sequences, useful in genetic testing and
                                                                                                                       Human silent SNP containing nucleic acid SEQ:2780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 901; 2653pp; English.
                                                                                                                                                                                                                                                                                                                                                   30-NOV-1999; 99US-0168138.
29-NOV-2000; 2000US-0726173.
                                                                                                                                                                                                                                                                                                                      30-NOV-2000; 2000WO-US32758.
                         AAI75839 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WP1; 2001-356160/37.
                                                                                                                                                                                                                                                        HO200140521-A2.
                                                                                                                                                                                                                          Homo saptens.
                                                                                                                                                                                                                                                                                       07-JUN-2001.
                                                                                          09-NOV-2001
                                                        AA175839;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the identification of nucleic acid molecules (AAI3913-AAI3114) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genese from a number (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype. The nucleic acids containing the polymorphic sites may be useful in forensics and paternity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype
                                      Caps
                                                                                                                                                                                                                                                                                                         Human; resequence; genotype; disease; forensic; paternity testing;
single nucleotide polymorphism; SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
replace(16,T)
/*tag= a
/*tag= *single nucleotide polymorphism*
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     Length 33;
                                  Indels
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Best Local Similarity 83.3%; Pred. No. 3.4e+04;
Matches 25; Conservative 0; Mismatches 5; Indels
Score 22.4; DB 24;
Pred. No. 2.8e+04;
0; Mismatches 6;
                                                                                                                                                                                                                                                                          Human single nucleotide polymorphism (SNP) 97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31 BP; 8 A; 11 C; 8 G; 4 T; 0 other;
                                                          1018 GAGCTCAAGCTGGCTGGCCTGGCCCG 1049
                                                                              32 GAGCTGAATTGGCTAATTTGGCCTGGCTG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cargill M, Ireland JS, Lander ES;
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                                                                                                                                                                                96
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22-MAY-2000; 2000US-0206129.
                                                                                                                                                                            AAI30264 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2001; 2001WO-US07268
                                                                                                                                                                                                                                           (first entry)
            Best Local Similarity 81.2
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                         18-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                         Variation
                                                                                                                                                                                                          AAI30264;
Query Match
                                                                                                                                             RESULT 4
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ANT3060 to ANT9867 represent isolated human polymorphic polynucleotide sequences (I), which contain single nucleotide polymorphisms (SNPs).

ANM31114 to ANM3129 represent peptides related to human polymorphic polymorphic contains sequences. The sequences can be used in gene and protein the represent peptides related to human polymorphic polymorphic contemps, and in vaccine production (I) and the polymorphic polymorphic coded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polymorphic polymorphic contemps, (I) may be used to treat disorders by rectifying mutations for detections in a patient's genome that affect the activity of contemps own production of polymorphic proteins or to supplement the patients are now production of polymorphic polymorphic societies complementary sequences may also be used as DNA probes in diagnostic contemps. The polymorphic patients may be used as antigens in the production of multibodies specific for polymorphic polymorphic polymorphic of high may also be used as diagnostic agents for detecting the resence of polymorphic polymorphic polymorphic polymorphic production of multipolies may also be used as diagnostic agents for detecting the presence of polymorphic polymorphic pagents for detecting the presence of polymorphic polymorphic pagents for detecting the pagents for detecting the pagents for detecting the pagents.
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tive 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1642 CGGCTGGAGGGATGCCACACCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 CIGCITGAGCGCTGCCACCCCTCTGGGGCCCCCC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50 BP; 7 A; 22 C; 13 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI29606 standard; DNA; 31 BP
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Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA129606;
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Gaps

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979 GACCTCAAGCCCCAGAACCTGCTCATCAAC 1008

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GACATCAAGCCCCAGAACCTGCTGGTGGAC 31

Length 31;

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The invention relates to a method of obtaining a stable transplastome, by transforming a recipient plastome (RP) with a polypuclectide having a 5' sequence homologous to a region of RP, and joined to it, a sequence requiatory region capable of securing expression of coding region in the regulatory region capable of securing expression of coding region in the plastid and joined to it, and a 3' sequence homologous to a region of RP. The method is useful for obtaining a transplastomic plastid, by transforming a plastome within a plastid such as proplastid, amyloplast, changolast, etioplast or leucoplast, preferably chloroplast. The method provides high, uniform, reliable expressed protein. The plants, with stable inheritance of the trait by avoiding the potential control and angerous spread of transgenes to the ecosystem. The present sequence represents a PCR primer for amplifying a info coding region, used in generating expression vectors for infin chloroplasts.
                                                                                                                                                                                                                                                                                            Obtaining a stable transplastome for producing a transplastomic c plant or seed, comprises transforming a recipient plastome with a polynucleotide comprising a 5' and 3' sequence homologous to the
                                                                                                                                                                        (ITGE-) INT CENT GENETIC ENG & BIOTECHNOLOGY.
                                                                                                                                                                                                               Reddy S, Sadhu L, Shukla V, Ferraiolo G;
                                                                                                                                                                                                                                                                                                                                                                                                      Example 12; Page 127; 128pp; English.
                                                               08-DEC-2000; 2000WO-BP12446.
                                                                                                         08-DEC-1999; 99GB-0029075.
                                                                                                                                                                                                                                                       WPI; 2001-381671/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200206497-A2.
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                       14 - JUN - 2001
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                                                                                                                                                                                                                                                                                                                                                                recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the identification of nucleic acid molecules (AA129513-AA131314) from the human genome which include polymorphic sites which can predispose individuals to disease. Warlous genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNP) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular penonyment or disporder (e.g. diabetes) associated with a particular genetype. The nucleic acids containing the polymorphic sites may be useful in forensics and paternity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules from the human genome which include polymorphic stes, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype
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                                                                               Human; resequence; genotype; disease; forensic; paternity testing; single nucleotide polymorphism; SNP; ss.
                                                                                                                                                                                                                                  /*tag- a
/standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plastome; plastid; chloroplast; transgene; plant;
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                                          Human single nucleotide polymorphism (SNP) PCTAIRE3 1.
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Local Similarity 80.6%; Pred. No. 4.9e+04;
ics 25; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31 BP; 6 A; 9 C; 8 G; 8 T; 0 other;
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                                                                                                                                                                                          Location/Qualifiers replace(16,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cargill M, Ireland JS, Lander ES;
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AM12223/C
ID AAH22523 standard; DNA; 42 BP
XX
AC AAH22523;
XX
DT 22-AUG-2001 (first entry)
XX
EPCR primer SR53 for amplifying
XX
Transplastome; plastome; plast
XX
KW
IfinG; PCR primer; ss.
XX
Synthetic.
XX
NO200142441-A2.
                                                                                                                                                                                                                                                                                                                                                                              07-MAR-2001; 2001WO-US0726B.
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22-NAY-2000; 2000US-0206129.
18-OCT-2001 (first entry)
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                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                               Variation
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Gaps
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                                              Length 42;
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lfnG coding region DNA amplifying PCR primer, SR53
                                         Ouery Match 1.24; Score 21.4; DB 22;
Best Local Similarity 80.64; Pred. No. 5.6e+04;
Matches 25; Conservative 0; Mismatches 6;
Sequence 42 BP; 15 A; 10 C; 11 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ITGE-) INT CENT GENETIC ENG & BIOTECHNOLOGY.
                                                                                                                                           270 ACGIGCIGCICCIGGGGAACTICGITCIGCA 300
                                                                                                                                                                    35 ACGTACGGGTCCTGGCGACCTTCGATCTGCA 5
                                                                                                                                                                                                                                                                                                                       95
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                                                                                                                                                                                                                                                                 RESULT 8
AAD29563/C
ID AAD29563 standard; DNA; 42
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Claim 28; Page 290; 587pp; English.
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27-JUN-1991;
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17-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                               AAQ69891).
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                                                                                                                                                  The patent discloses a method of producing a protein of interest which a movelves a expressing a polynucleotide fusion construct in a plastid to produce a fusion protein comprises a polynucleotide coding sequence of the protein of interest where the construct comprises a polynucleotide coding sequence of the protein of interest operably linked to a polynucleotide coding sequence of a fusion protein partner. The methods of the invention are useful for producing a cotive variant of interest which comprises a human protein or its biologically active variant or fragment, a pharmaceutically active protein, an IFN (interferon), its biologically active variant or fragment, a human IFN (interferon), its biologically active variant or fragment, a human IFN (interferon) its biologically active variant or fragment, a human IFN (interferon) its biologically active variant or fragment, a human IFN (interferon) its biologically active variant or fragment, a human IFN (interferon) its biologically active variant or fragment, a human IFN (interferon) is useful for the generation of transplastomic plant cells, plants and seades The protein of interest obtained by the methods of the invention is useful for the menufacture of a medicament for treating convention is useful for the menufacture of a medicament for treating convention is useful for the menufacture of a medicament for treating convention is useful for the menufacture of a medicament for treating convention is useful for the menufacture of a medicament for treating convention is useful for the menufacture of a medicament for the menufacture of a leases organization of the invention in the sequence is a PCR primer which the acemplification of the invention to generate pdusing expression convention is under for inforced in the invention to generate pdusing active convention is under for inforced in the invention to generate pdusing active convention is under for an inforced in the invention to generate pdusing active construction is under for a medicament for treating ac
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                                           Producing a protein of interest, e.g., a pharmaceutically active protein, comprises expressing a polynucleotide fusion construct in a plastid and producing a fusion protein comprising the protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA protein-binding assay; test sequence; screening sequence; promoter; target; TATA box; Herpes Simplex Virus; HSV; origin of replication; UL9; transcription factor; TFIID; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 1.24; Score 21.4; DB 24; Length 42; Local Similarity 80.64; Pred. No. 5.6e+04; cs 25; Conservative 0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 42 BP; 15 A; 10 C; 11 G; 6 T; 0 other;
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                                                                                                                        Example 1; Page 90; 92pp; English.
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930S-0123936
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              WPI; 2002-171810/22.
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17-SEP-1993;
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Libraies of synthetic or blological cpds. for their ability

Libraies of synthetic or blological cpds. for their ability

to bind DNA test sequences. The assay is versatile in that any

conditions of test sequences can be tested by placing the test sequence

adjacent to a defined protein-binding screening sequence. Binding

adjacent to a defined protein-binding screening sequence. Binding

confined the protein mol. to its cognate binding sequence. When such a mol.

Confined the test sequences, the equilibrium of the DNA: protein complexes

Confined the test sequences in the concentration of free DNA probe.

Confined the sequences adjacent to the binding site for the evaryotic

confined the sequences adjacent to the binding site for the evaryotic

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confined the sequences adjacent to the binding site for the evaryotic

confined the sequences adjacent to the binding site for viral genes.

The test sequences may also be randomly generated. DNA: protein

confined the sequences may also be randomly genesa, e.g. the Herpes Simplex

Vivia (HSV) oxigin of replication and UL9 (see AAQ69851-52, AAQ69865 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duplex DNA; target region; binding characteristic; DNA binding protein; TFIID; transcription factor; binding site; inhibition; enhance; cancer; inherited genetic disorder; alpha-D-galactosidase A; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.24; Score 21.4; DB 15; Length 46; Best Local Similarity 71.84; Pred. No. 5.8e+04; Matches 28; Conservative 0; Mismatches 11; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Turin LM;
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91US-0723618.
92US-0996783.
93US-0123936.
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Test sequences that are used in the method of the invention of determining the DNA sequence preference of a DNA-binding molecule. The method comprises: (1) adding a test molecule and a DNA-binding molecule. The method comprises: (1) adding a test molecule and a DNA-binding protein to a mixture of duplex DNA test oligonucleotides, each of the test colligonucleotides having a test sequence adjacent to a screening sequence. Where the screening sequence brinds to the DNA-binding protein with a binding affinity that is independent of the DNA-binding protein with a collidos several test sequences; (11) incubating the test molecule, the mixture of duplex DNA test oligonucleotides and the sufficient to permit binding of the test molecule to test of a time sufficient to permit binding of the test molecule to test of a time sufficient to permit binding of the test molecule to test of a time sufficient to permit binding of the test molecule to test of the minute sufficient to permit binding of the test molecule to test of the minute sufficient to permit binding of the test molecule to test of the minute sufficient to permit binding of the test molecule to test of the minute of the unbound test oligonucleotides. Colligonucleotides from test oligonucleotides. Test sequences (11) to (1v); (vi) isolating the minute of the min
                                    Sequences AAX17001 to AAX17600 represent specifically claimed target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        // Match 1.2%; Score 21.4; DB 20; Length 46; Local Similarity 71.8%; Pred. No. 5.8e+04; hes 28; Conservative 0; Mismatches 11; Indels (
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Matches
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                                 The sequences given in AAT63713-4312 represent duplex DNA's which act as target regions in the method of the invention. The method for attering the binding characteristics of a DNA-binding protein to duplex DNA with a small molecule which binds sequence-specifically to a target region, where, when the small concerned is bound to the target region, where, when the small concerned is bound to the target region, where, when the small concerned by more than 4 bp, a binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the control of the DNA. The binding protein, pref. TFIID, to its binding site on the duplex DNA. The binding protein, pref. TFIID, to its binding site. The compounds isolated using this method are potentially useful as therefore the binding of the DNA-binding protein to its binding site. The compounds isolated using this method are potentially useful as therefore the binding determination of sequence-specific and relative constitutions of known DNA-binding agents for different DNA sequences. The method is suitable for screening large biological or chemical constitution of these duplex DNA's allows a single DNA-protein interaction to be used for screening sequence-specific, or preferential, DNA binding proteins that recognise almost any possible sequence (see also ANT49339-
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71.8%; Pred. No. 5.8e+04;
tive 0; Mismatches 11;
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Claim 6; Column 177-178; 264pp; English.
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91US-0723618.
92US-0996783.
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95US-0475228
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17-SEP-1993;
07-JUN-1995;
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27-JUN-1991;
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Gaps

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Decreasing transcriptional activity of genes for treating infections or cancer, by administration of an agent that binds to two non-overlapping regions of the gene
                                                                                                                                                                 DNA binding molecule screening; inhibition of transcription; infection; human immunodeficiency virus; HIV; parasite: cancer; cardiovascular; respiratory; gastrointestinal; endocriue; metabolic; rheumatic; immunological; haematological; neurological; psychiatric; dermatological; ophthalmological; musculo-skeletal; urogenital disorder; ss.
                                                                                                                                            DNA binding molecule screening method test sequence #156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fry KE;
2 GCGGTGGATTGGACGCTCCACCATCACAGGGCAGCGCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Turin LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cantor CR, Andrews BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                92US-0996783.
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                                                                     ABK82647 standard; DNA; 46
                                                                                                                    27-AUG-2002 (first entry)
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23-DEC-1992;
17-SEP-1993;
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us-10-017-621-3.lim50.rng

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contain single nucleotide polymorphisms (SNPs). A method is included in the invention for analysing a nucleic acid sample, which consists of determining the base occupying an uncleic acid sample, which consists of the SNP containing sequences. The nucleotide sequences can be used in the diagnosis or monitoring of diseases, such as cancer, inflammation, heart diseases, of monitoring of diseases, such as cancer, inflammation, heart diseases, and so a pharmaceutical system, and infection by microorganisms. The oligonocicotides are also useful in the manufacture of a medicament for the treatment or prophylaxis of the diseases, and as a pharmaceutical. SNP containing oligonucleotides are useful in medicine and genetic analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46 BP; 7 A; 13 C; 18 G; 6 T; 2 other;
                                                                                                                                                                                                                                                                                            702 CAAGGAGATCAGACTGGAACA 722
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                                                                                                                                                                                                                                                                                                                | CAAGGAGATCAGACTGGAACA 21
                                                                                                                                                                                                                                                                                                                                                                                                       AAH70659 standard: cDNA; 46
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14-NAR-2000; 2000US-0189315.
12-NAX-2000; 2000US-0203791.
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21-JUL-2000; 2000US-0220114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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21-DEC-1999;
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                                                                                                                                                                                                                                                                                                                         윱
                                       The invention relates to a method of decreaing transcriptional activity contacting (TI) with a binding agent comprising contacting (TI) with a binding agent comprising contacting (TI) with a binding agent comprising to contacting (TI) with a binding agent comprising to the small duplex binding molecule that binds to a non-overlapping region of target binding molecule that binds to a non-overlapping region of target contacting for inhibiting transcription of a sequence (TS). The method is useful for inhibiting transcription of a range of disease-related genes for treating infections (by viruses, not cludy human immunodeficiency virus, bacteria, fungi, protozoa and parasites), cancer, cardiovascular, respiratory gastrointestinal, and parasites), cancer, cardiovascular, respiratory gastrointestinal, candocrinc/metabolic, rheumatic/dimunological, hematological, musculo-skeletal, genetic or urogenital departs of pathological genes sequence-specific inhibition of transcription of pathological genes transcription affecting affecting transcription of cellular genes regulated by the same than a fafecting and can be applied to regulated by the same and the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NA sequences AAH62100 - AAH62688 represent segments of human genes which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid segments of the human genome, particularly from genes including polymorphic sites, for phenotype correlation, forensics, paternity testing, medicine and genetic analysis
                                                                                                                                                                                                                                                                                                                                                                                                     Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single nucleotide polymorphism; SNP; human; cancer; inflammation; heart disease; paternity testing; forensic science; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
replace(11,G)
/*teg- a
/standard_name- 'single nucleotide polymorphism'
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                                                                                                                                                                                                                                                                                                                                                         Match 1.2%; Score 21.4; DB 24; Length 46; Local Similarity 71.8%; Pred. No. 5.8e+04; Hes 28; Conservative 0; Mismatches 11; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCTAIRE-1 polymorphism containing DNA fragment #96.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GCGGTGGATTGGACGCTCCACCAATCACAGGGCAGCGC 40
                                                                                                                                                                                                                                                                                                                            Sequence 46 BP; 9 A: 14 C; 16 G; 7 T; 0 other;
            Example 15; SEO ID No 156; 98pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cervical cancer; cytostatic: pre-malignant condition; gene therapy; ss.
                                                                                                                                       Caps
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                                                                                                                                    ö
                                                                         Length 21;
                                  Score 21; DB 22; Length 41; Pred, No. 5.4e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cervical cancer marker nucleic acid 1933.
Sequence 21 BP; 9 A; 4 C; 6 G; 2 T; 0 other;
                                                       Query Match 1.2%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 5.4 Matches 21; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schlegel R, Deeds J, Berger A, 2hao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 415; 1051pp; English.
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Length 46;

DB 22;

1.2%; Score 21;

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The present invention relates to oligonuclectides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoletin, cappatosis related proteins, cacherin, cyclin, polymerase, uncogenes, histones, kinses, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, coprotein coupled receptors and thiosesterases. The present sequence is one such oligonuclectide. The oligonucleotides and the peptides encoded diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, disgnossed and/or treated include clisases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes.

CC systemic lupus erythromatosus and Grave's diseases) inflammation, cancer concerns of the bladder, brain, breast, colon and kidney,
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                                                                                                                                                                                                                                                                                                                            Immunosuppressive: immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptools related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; colony stimulating factor; intecfleukh; Gyptotin coupled receptor; thioesterase; inflammation; nervous system disease; autoimmune disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autolmmune diseases and infections -
                          Gaps
                        ő
                      Indels
Best Local Similarity 71.1%; Pred. No. 7.3e+04;
Matches 27; Conservative 0; Mismatches 11;
                                                    550 AAGCCCTCAGCCGCCGCCTCGTCTCAGCCTATC 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50 BP; 1 A; 27 C; 11 G; 11 T; 0 other;
                                                                           41 AAGCGTCTCTGCAGCCGCCCCCCGGGGGTGCTCCTATC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 3547; 4143pp; English.
                                                                                                                                                                                                                                                                                              Human SNP oligonucleotide #7494.
                                                                                                                                                                AAL34286/c
ID AAL34286 standard; DNA; 50 BP.
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27-DEC-2000; 2000US-0173419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-465210/50.
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Gaps

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Query Match
1.2%; Score 21; DB 22; Length 50;
Best Local Similarity 66.7%; Pred. No. 7.6e+04;
Matches 30; Conservative 0; Mismatches 15; Indels

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208 GAGCAGATAGGCCTGGATGAGAGTGGTGGTGCTGCCGGCGCAGTGAC 252
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Search completed: March 3, 2003, 22:46:23 Job time : 431 secs

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Page 1

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model	
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Title: US-10-017-621-3 Perfect score: 1745 Sequence: 1 tygaagcagcgtaaaggatggttcacctgcccacttgtcc 1745	
Scoring table: IDENTITI_NUC Gapop 10.0 , Gapext 1.0	·.
Searched: 2054640 seqs, 14551402878 residues ,	
Total number of hits satisfying chosen parameters: 841850	
Minimum DB seg length: 0 Maximum DB seg length: 50	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Detabase : GenEmbl:* 2	

Pred. No. is the number of results predicted by chance to have a

REFERENCE AUTHORS TITLE JOURNAL

RESULT 1
HSHCAK
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOUNCE
ORGANISM

PRI 08-AUG-1995

ALIGNMENTS

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Homo sapiens
Eukaryota: Metazoa; Chordata; Cranlata: Vertebrata: Buteleostomi;
                                                                                                                                                                                                            Rose-John, S.
CONUTORATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS
PATENT: NO 9722891-A 9 12-SEP-1997;
ANGEWANDIE GENTECHNOLOGIE SYST (DE); ROSE JOHN STEFAN (DE)
Location/Qualifiers
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Avraham, H. Karsenty. and Godowski, P.J.
Wethods and Kits using macrophage stimulating protein
Patent: US 5696086-A 5 09-DEC-1997;
Location/Qualifiers
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69.8%; Pred. No. 1.8e+06;
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        50 CAGAACCTCCACCTCCAGAACCTCCACCTCCAGAACCTCCACCTCCTCGA 1
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Local Similarity 66.7%; Pred. No. 1.6e+06;
hes 32; Conservative 0; Mismatches 16;
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Sequence 2780 from Patent W00140521.
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Sequence 5 from patent US 5696086.
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184671.1 GI:3022191
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/db_xref="taxon:32644"
26 c 4 9
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                                                              3 (bases 1 to 49)
Wu,L., Yee, Liu,L., Carbonaro-Hall,D., Venkatesan,N., Tolo,V.T.
and Hall,F.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Division of Orthopaedic Surgery, 4650 Sunset Boulevard, Los
Angeles, CA, 90027, USA
2 (bases 1 to 49)
Wu.L. and Hall,F.L.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONJUGATE FOR MODIFYING INTERACTIONS BETWEEN PROTEINS PACENT: NO 973281-A 8 12-SEP-1997;
ANGEWANDIE GENTECHNOLOGIE SYST (DE); ROSE JOHN STEFAN (DE)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 49;
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                                                                                                                      Molecular cloning of the human CAK1 gene encoding a cyclin-dependent kinase-activating kinase oncogene 9 (7), 2089-2096 (1994) 94268852
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1.4%; Score 23.8; DB 9; Length 46
Best Local Similarity 72.1%; Pred. No. 7.8e+05;
Matches 31; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                            /note="catalytic subunit; subdomain VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="protein kinase"
/protein_id="CAA33766.1"
/db_xref="G:1939888"
/db_xref="G:1939888"
/translation="kWSSKTGRRWFGIFW"
a 8 c. 12 g 15 t
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/organism-"unidentified"
/db_xxef="taxon:32644"
a 4 c 26 g 13
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A93721
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=2
                                                                                                                                                                                                                                                                                                                                       /gene="HCAK"
<1. .>49
/gene="HCAK"
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Rose-John, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unidentified
unclassified.
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ORIGIN
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JOURNAL
REFERENCE
AUTHORS
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PUBMED
FEATURES
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A93721/c
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Gaps

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Patent: WO 0142441-A 53 14-JUN-2001;
International Centre for Genetic Engineering and Blotechnology (IT)
Location/Qualifiers
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Patent: WO 0206497-A 53 24-JAN-2002;
International Centre for Genetic Engineering and Blotechnology (IT)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.
1 (bases 1 to 46)
Edwards.C.A., Cantor.C.R., Andrews.B.M., Turin,L.M. and Fry,K.E.
Method of determining DNA sequence preference of a DNA-binding
molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.2%; Score 21.4; DB 6; Length 42; Best Local Similarity 60.6%; Pred. No. 2.80+06; Matches 25; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                          / Match 1.2%; Score 21.4; DB 6;
Local Similarity 80.6%; Pred. No. 2.8e+06;
Nes 25; Conservative 0; Mismatches 6;
                                                                                       1, .42
/organism-"synthetic construct"
/db_xref="taxon:32630"
/note="primer" | 9 6 t
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/db_xref="taxon:32630"
/note-"primer."
1 0 c 11 g 6 t
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AR032544
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Location/Qualifiers
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Sequence 53 from Patent W00206497.
AX382049
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AX382049/c
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TITLE
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TITLE
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AR032544
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                     1 (bases I to 50)
Shinkete, R.A. and Caach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 01405211A 2780 07-JUN-2001;
Curagen Corporation (US)
Location/Qualiflers
                                                                                                                                                                                                                                                                     25. .26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg42460243*
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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synthetic construct
synthetic solutions
synthetical sequences.
1 (base 1 to 42)
Reddy, S. I., Sadhu, L. I., Shukla, V.C. and Ferralolo, G. I.
Plastid transformation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22; DB 6; Length 50;
Pred. No. 2e+06;
0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX248673 31 bp DNA Sequence 752 from Patent W00166800,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
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/Organism-"Homo sapiens"
/db_xref-"taxon.9606"

1 a 11 c 7 g 4
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Sequence 53 from Patent W00142441.
AX182243

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    /organisme"Homo sapiens"
    /db_xrefe"taxon:9606*

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2 GACATCAAGCCCCAKAACCTGCTGGTGGAC 31
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1,3%;
Best Local Similarity 73.7%;
Matches 28; Conservative
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AX182243/c
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ACCESSION
VERSION
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ORIGIN
                                           AUTHORS
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AUTHORS
TITLE
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AX248673
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SOURCE
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PAT 18-MAR-2002

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Indels

Length 42;

PAT 29-SEP-1999

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Gaps

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REFERENCE AUTHORS TITLE

JOURNAL FEATURES PAT 28-SEP-2001

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 46)
2 (bases 1 to 46)
2 (beds, J., Berger, A. and Zhao, X.
Genes, compositions, X. kits, and methods for identification,
àssessment, prevention, and therapy of cervical cancer
Patent: WO 0143467-A 1933 14-JUN-2001;
Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
1. 46
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Enkaryota; Metazoa; Chordata; Craniata; Vartebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 31)
Cargill, M.; Ireland, J.S. and Lander, E.S.
Human single nucleotide polymorphisms
Patent: WO 0166800-A 94 13-SEP-2001;
WHITEHEAD INSTITUTE FOR BIONEDICAL RESEARCH (US)
                                                 i (bases i to 46)
Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
Screening assay for the detection of DNA-binding molecules
Patent: USC 175014-A 156 10-MAR-1998;
Location/Qualifiers
                                                                                                                                                                                                                            1.2%; Score 21.4; DB 6; Length 46; 71.8%; Pred. No. 2.8e+06; tive 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 1.2%; Score 21; DB 6; Length 31;
Local Similarity 77.4%; Pred. No. 3.5e+06;
nes 24; Conservative 1; Mismatches 6; Indels
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Db 2 GCGCTGGATTGGACGCTCCACCAATACACAGGCAGCGCC 40
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AX186238.1 GI:15137666
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Sequence 94 from Patent WO0166800.
AX248015
AX248015.1 GI:15862638
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/db_xref="taxon:9606"
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In (bases 1 to 46)

Rewards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.

Sequence directed DNA binding molecules compositions and methods

Patent: US 6384208-A 156 07-MAX-2002;

Location/Qualifiers
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Edwards,C.A., Cantor,C.R., Andrews,B.W., Turin,L.W. and Fry,K.E.
Edwards,C.A., Cantor,C.R., Andrews,B.W., Turin,L.W. and Fry,K.E.
Sequence-directed DNa-binding molecules compositions and methods
Patent: US 5578444-A 156 26-NOV-1996;
Location/Qualifiers
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Sequence 156 from patent US 5726014.
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190558.1 GI:3935428
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Sequence 156 from patent US 5578444.
129284.1 GI:1820075
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Sequence 156 from patent US 6384208.
AR209208.1 GI:21510563
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                            2 others
                                                            Query Natch 1.2%; Score 21; DB 6; Length 46; Best Local Similarity 71.1%; Pred. No. 3.5e+06; Matches 27; Conservative 0; Mismatches 11; Indels
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LISM unidentified.
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LAUCE i (dases I to 46)
AHORS Hegemann.P.
ALLE METHOD FOR PRODUCING NUCLEIC ACID POLYMERS
OURNAL Patent: WO 9910358-A 24 04-MAR-1999;
RATURES LOCATION/Qualifiers
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And Andrea (Abbarref Taxon) 226.8; DB / 9e+/
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Sequence 24 from Patent WO9910358.
A98791 1 GI:6781812
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/db_xref="taxon:9606"
7 a 13 c 18 g 6
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Search completed: March 4, 2003, 00:06:28 Job time: 4794 secs

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| S1052/gcgdata/geneseqy-emb2/Nh1981.0hr; |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human SNP oligonne	Ruman Cdk5 related	Human Cdk5 related	Human single nucle	Human silent SNP c	Human single nucle	PCR primer SR53 fo	ifnG coding region	Human H1 histone g
SUMMARIES	AAL34335	ABA04099	ABA04100	AAI30264	AAI75839	AA129606	AAH22523	AAD29563	AAQ69406
99	2	34	24	2	22	22	22	24	15
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& Query Match	1.4	1.3	1.3	1.3	1.3	1.2	1.2	1.2	1.2
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Human H1 histone g Test sequence from Na bidding molecu PCTAIRE-1 polymorp Human SRP oligonuc BE19736591 primer RT-PCR primer/prob Primer 143 for hum Human SRP oligonuc Xcds1 degenerate p HIV POLISM mutage PCR primer for ser Primer for amplify Human qroton-adeno Human proton-adeno Human lerge protet IL-6 R and IL-6 tus Human SNP oligonuc Human SNP oligonuc Human A2D adenosin Human adenosine A2 Luw adenosine A2 Luw adenosine A2 Luw adenosine A1 Human adenosine A2 Luw adenosine A1 Human adenosine A2 Luw adenosine A1 Human adenosine A1 Luwan A1 Lu	tiinflammatory rapy, vaccine; related prote inase; colony kinosin; cytok thosaterase; thiosaterase; se; infection;
AANTG3868 AAX17156 AAK2195 AAK2295 AAK22936 AAK22936 AAK22936 AAK22936 AAK27936 AAK27936 AAK27936 AAK27936 AAK27936 AAK27936 AAK27936 AAK3795	ALIGNMENT ALIGNMENT "" " " " " " " " " " " " " " " " " "
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Sequence 33 BP; 10 A; 11 C; 6 G; 6 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; beta-amyloid; cyclin-dependent kinase inhibitor; nerve cell;
amyloid precursor protein; APP; Cdk5; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Cdk5 related PCR primer SEQ ID NO:18.
                                                                                                         Claim 1; Page 3563; 4143pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-2000; 2000JP-0131037.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA04099 standard; DNA; 33
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Shimkets RA, Leach M;
                         WPI; 2001-465210/50.
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The present invention describes medicinal compositions (1) inhibiting beta-amyloid production comprising an active component a substance that inhibits the activity of cyclin-dependent kinase (CDK). Also described are: (1) a method for screening compounds for their ability to inhibit the production of beta-amyloid by contacting with beta-amyloid producing cells; and (2) screening kits. (I) have nootropic and neuroprotective activities. (I) suppress the phosphorylation of amyloid precursor protein (APP) which is an essential step in the production of beta-amyloid. (I) can be used in the treatment and prevention of neurodegenerative diseases such as demontia and Alzhaimer's disease. The present sequence represents invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 22.4; DB 24
Pred. No. 2.8e+04;
0; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Cdk5 related PCR primer SEQ ID NO:19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1018 GAGCTCAAGCTGGCTGACTTTGGCCTGGCCCG 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GAGCTGAAATTGGCTAATTTTGGCCTGGCTCG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawabata S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 23; 62pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (YAMA ) YAMANOUCHI PHARM CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 1.3%;
Local Similarity 81.2%;
nes 26; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2001; 2001WO-JP03555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-APR-2000; 2000JP-0131037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA04100/c
ID ABA04100 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suzuki T, Watanabe T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-026209/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WOZ00182967-A1.
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Matches
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(first entry)

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Polymorphic nucleic acid sequences, useful in genetic testing and
                                                                                                                                                                  Human; single nucleotide polymorphism; SNP; genome; gene there
protein therapy; vaccine; probe; diagnostic assay; detection;
quantitation; restorative therapy; polymorphic; ds.
                                                                                                                                    Human silent SNP containing nucleic acid SEQ:2780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 901; 2653pp; English.
                                AAI75839 standard; DNA; 50 BP
                                                                                                                                                                                                                                                                                                                                                                        30-NOV-1999; 99US-0168138.
29-NOV-2000; 2000US-0726173.
                                                                                                                                                                                                                                                                                                                                      30-NOV-2000; 2000WO-US32758
                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-356160/37.
                                                                                                                                                                                                                                                                    WO200140521-A2.
                                                                                                                                                                                                                                      Homo saptens.
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                                                                                                  09-NOV-2001
                                                                AAI75839;
RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype
                                               Caps
                                                                                                                                                                                                                                                                                                                               Human; resequence; genotype; disease; forensic; paternity testing; single nucleotide polymorphism; SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= "single nucleotide polymorphism"
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             Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Match 1.3%; Score 22; DB 22; Length 31;
Local Similarity 83.3%; Pred. No. 3.4e+04;
ies 25; Conservative 0; Mismatches 5; Indels
                                           Indels
             DB 24;
                                             .
9
       Query Match 1.3%; Score 22.4; DB 24 Best Local Similarity 81.2%; Pred. No. 2.86+04; Matches 26; Conservative 0; Mismatches 6.
                                                                                                                                                                                                                                                                                             Human single nucleotide polymorphism (SNP) 97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31 BP; 8 A; 11 C; 8 G; 4 T; 0 other;
                                                                     1018 GAGCTCAAGCTGGCTGACTTTGGCCTGGCCCG 1049
                                                                                        (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualiflers
replace(16,T)
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22-MAY-2000; 2000US-0206129.
                                                                                                                                                                                         AAI30264 standard, DNA; 31
                                                                                                                                                                                                                                                           18-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                  Homo saptens
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Variation
                                                                                                                                                                                                                            AAI30264;
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                                                                                                                                                                             AAI30264
                                                                                                                                                          RESULT
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AM5131060 to AM179867 represent isolated human polymorphic polynucleotide sequences (1). Which contain single nucleotide polymorphisms (SNPS).

AM51314 to AM51329 represent peptides related to human polymorphic polymorphic contents. The sequences can be used in gene and protein contents and in vaccine production. (1) and the polypeptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of polymorphic polypeptides. CC for example, (1) may be used to treat disorders by rectifying mutations or cleations in a patient's genome that affect the activity of polypeptides by expressing inactive proteins or to supplement the patients and production of polypeptide. Additionally, (1) and its complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic in samples, and therefore which patients may be in need of restorative contents. The polypeptides encoded by (1) may be used as antigens in the production of matibodises may also be used to down regulate expression and activity.

The antibodies may also be used as diagnostic agents for detecting the presence of polymorphic polypeptides in samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 1.3%; Score 22; DB 22; Length 50 Local Similarity 73.7%; Pred. No. 4.2e+04; nes 28; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1642 CGCTGGAGGGATGCCACACCCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 50 BP; 7 A; 22 C; 13 G; 8 T; 0 other;
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Matches
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AAI29606
ID AAI29
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AC AAI29
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Gaps

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979 GACCTCAAGCCCCAGAACCTGCTCATCAAC 1008

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Best Local

2 GACATCAAGCCCCAGAACCTGCTGGTGGAC 31

13-SEP-2001.

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The invention relates to a method of obtaining a stable transplastome, by transforming a recipient plastome (RP) with a polynucleotide having a copy transforming a recipient plastome (RP) with a polynucleotide having a copy of RP. The method specific to a region of RP. Indeed to it, a sequence copy and the copy of th
                                                                                                                                                                                                                                                                                                                                                                                         Obtaining a stable transplastome for producing a transplastomic cell, plant or seed, comprises transforming a recipient plastome with a polynucleotide comprising a 5' and 3' sequence homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transgenic plant; transplastomic plant; medicament; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ifnG coding region DNA amplifying PCR primer, SR53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21.4; DB 22;
Pred. No. 5.6e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 42 BP; 15 A; 10 C; 11 G; 6 T; 0 other;
                                                                                                                                                                                                                                (ITGE-) INT CENT GENETIC ENG & BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.2%; Sco...
80.6%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ITGE-) INT CENT GENETIC ENG & BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                  Reddy S, Sadhu L, Shukla V, Ferraiolo G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 ACGIGCICCICCIGGGGAACTICGITCIGCA 300
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AAD29563/c
ID AAD29563 standard; DNA; 42 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUL-2000; 2000GB-0017397.
                                                                                    08-DEC-2000; 2000WO-BP12446.
                                                                                                                                         08-DEC-1999; 99GB-0029075.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.6
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                          WPI; 2001-381671/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200206497-A2.
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                               14 - JUN - 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to the identification of nucleic acid molecules (AAI29513-AAI31314) from the human genome which include polymorphic sites which can prediapose individuals at disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diaberes) associated with a particular genotype. The nucleic acids containing the polymorphic sites may be useful in forcesics and paternity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                Human; resequence; genotype; disease; forensic; paternity testing;
single nucleotide polymorphism; SNP; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transplastome; plastome; plastid; chloroplast; transgene: plant;
ifnG; PCR primer; ss.
                                                                                                                                                                                                                                                                                                              /*tag= a
/standard_name= "single nucleotide polymorphism"
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                                                        Human single nucleotide polymorphism (SNP) PCTAIRE3 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer SR53 for amplifying a 1fnG coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31 BP; 6 A; 9 C; 8 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        577 GTCAGCCTATCTGAGATTGGCTTTGGGAAAC 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                      Location/Qualiflers replace(16,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cargill M, Ireland JS, Lander ES;
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ID AAH22523 Standard; DNA; 42 BP
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22-MAY-2000; 2000US-0206129.
   (first entry)
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Matches 25; Conserv
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18-OCT-2001
                                                                                                                                                                                                    Homo sapiens
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Synthetic.

AAH22523;

RESULT 7

Query Match

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testing.

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Gaps

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Length 42; Indels

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The patent discloses a method of producing a protein of interest which involves a expressing a polynucleotide fusion construct in a plastid to produce a fusion protein comprising the protein of interest where the construct comprises a polynucleotide coding sequence of the protein of interest operably linked to a polynucleotide coding sequence of a fusion protein of interest which comprises a human protein or its biologically active variant or fragment, a pharmaceutically active protein, a buman iFN clinkerferon, its biologically active variant or fragment, a human iFN clinkerferon, its biologically active variant or fragment, a human iFN clinkerferon, its biologically active variant or fragment, a human iFN clinkerferon of transgenic plants. Nethods of the invention are useful for the generation of transplastomic plant cells, plants and seeds. The protein of interest obtained by the methods of the invention is useful for the manufacture of a medicament for treating a disease condition. The present DNA sequence is a PCR primer which the exemplification of the invention to generate pGUSIFNG expression continued in chloroplasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                              Producing a protein of interest, e.g., a pharmaceutically active protein, comprises expressing a polynucleotide fusion construct in plastid and producing a fusion protein comprising the protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 1.2%; Score 21.4; DB 24; Length 42; Best Local Similarity 80.6%; Pred. No. 5.6e+04; Matches 5; Conservative 0; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA protein-binding assay; test sequence; screening sequence promoter; target; TATA box; Herpes Simplex Virus; HSV; origin of replication; UL9; transcription factor; TFIID: ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fry KE, Turin LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence-directed DNA-binding molecules · useful in pharmaceuticals and as molecular reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42 BP; 15 A; 10 C; 11 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human H1 histone gene FNC16, target region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 ACGTGCTGCTCGTGGGAACTTCGTTCTGCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Edwards CA,
                                                                                                                                                                                                                                             Example 1; Page 90; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ69406 standard; DNA; 46 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            920S-0996783;
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WPI; 2002-171810/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-DEC-1992;
17-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ69406;
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A DNA protein-binding assay is provided, useful for screening
Libraries of synthetic or biological cpds. for their ability
to bind DNA test sequences. The assay is versatile in the any
to bind DNA test sequences. The assay is versatile in the any
adjacent to a defined protein-binding screening sequence.
Binding
of mols. to these test sequences changes the binding characteristics
of the protein mol. to its cognate binding sequence. When such a mol.
binds the test sequence, the equilibrium of the DNA protein complexes
is disturbed, generating changes in the concentration of free DNA probe.
One application of this method is to eucaryotic general transcription
factors (e.g. FTID), whate the larget region is typically selected
from DNA sequences adjacent to the binding site for the eucaryotic
transcription factor. Numerous exemplary test sequences are given:
the sequences in And69251771 and AAN69860 correspond to promoter
targets (typically, TATA box-condy. sites) for human genes and the
sequences in AAN69312-849 correspond to promoter targets for viral genes.
The test sequences may also be randomly generated. DNA:protein
interaction may be used for screening purposes, a.g. the Harpes Simplax
and the sequences may even for screening purposes, a.g. the Harpes Simplax
and the sequences are protein and UL9 (see AAN669865 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duplex DNA; target region; binding characteristic; DNA binding protein; TFIID; transcription factor; binding site; inhibition; enhance; cancer; inherited genetic disorder; alpha-0-galactosidase A; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Altering binding characteristics of DNA binding proteins to duplex DNA - by attaching specific small cpd. to target region close to the protein's binding site, useful in treatment of viral disease, cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2%; Score 21.4; DB 15; Length 46; 71.8%; Pred. No. 5.8e+04; tive 0; Mismatches 11; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human H1 histone gene FNC16 gene TFIID binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1641 GCGCTGGAGGGATGCCACACCCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GCGGTGGATTGGACGCTCCACCAATCACAGGGCAGCGCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46 BP; 9 A; 14 C; 16 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fry KE,
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                          Claim 28; Page 290; 587pp; English.
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920S-0996783.
930S-0123936.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 71.8 es 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Andrews BM, Cantor CR,
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13-DEC-1992;
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Matches
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AAT63868
ID AAT6
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     The sequences given in AA763713-4312 represent duplex DNA's which act as target regions in the method of the invention. The method for altering the bindading characteristics of a DNA-binding protein to duplex DNA with a small molecule which hids sequence-specifically to a target region, where, when the small molecule is bound to the target region, where, when the small molecule is bound to the target region, where, when the small colocule is added at a concentration effective to alter the power lapping by more than 4 bp. a binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the binding of the DNA-binding protein. Pref. TFIID, to its binding site on the duplex DNA. The binding protein protein to its binding site on the compounds isolated using this method are potentially useful as therefore the binding of the bunding protein to its binding site. The compounds isolated using this method are potentially useful as the method is suitable for screening large biological or chemical compounds of screening large biological or chemical increations of sequence-specific and relative the area duplex DNA's allows a single DNA:protein interaction to be used for screening sequence specific, or preferential, DNA binding compounds that recognise almost any possible sequence (see also ANT49539-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determination of DNA sequence preference of a DNA-binding molecule based on inhibition of binding of protein to oligonucleotide sequence attached to test sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Test sequence; DNA-binding molecule; screening sequence; human; nucleic acid amplification; target; viral; ds.
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                                                                                                                                                                                                                                                                                                                                                                                    1641 GCGCCTGGAGGGATGCCACACCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                 2 GCGGTGGATTGGACGCTCCACCAATCACAGGCAGCGCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Test sequence from human H1 histone gene FNC16.
                                                                                                                                                                                                                                                                                                          Sequence 46 BP; 9 A; 14 C; 16 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Columns 179-180; 270pp; English,
Claim 6; Column 177-178; 264pp; English.
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91US-0723618.
92US-0996783.
93US-0123936.
95US-0475228.
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                                                                                                                                                                                                                                                                                                                                              Similarity 71.8
28; Conservative
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27-JUN-1991;
23-DEC-1992;
17-SEP-1993;
07-JUN-1995;
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Matches 2
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AAX17156
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test sequences AAX17001 to AAX17600 represent specifically claimed target
test sequences that are used in the method of the invention of
determining the DNA sequence preference of a DNA-binding molecule. The
method comprises: (1) adding a test molecule and a DNA-binding protein to
a mixture of duplex DNA test oligonuclectides, each of the test
coligonuclectides having a test sequence adjacent to a screening sequence binds to the DNA-binding protein with a
coligonuclectides having a test sequence of bunding affinity that is independent of the DNA sequence, and where the mixture of duplex DNA test coligonuclectides
includes several test sequences; (11) incubating the test molecule, the
mixture of duplex DNA test oligonuclectides and the DNA-binding protein
coligonuclectides from test oligonuclectides and the DNA-binding protein;
coligonuclectides from test oligonuclectides; (v) repeating steps
colity; (vi) isolating the amplified test oligonuclectides; and
colity; (vi) isolating the amplified test oligonuclectides; and
colity; (vi) sequences AAX17482-X17599 correspond to promoter targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Decreasing transcriptional activity of genes for treating infections or cancer, by administration of an agent that binds to two non-overlapping regions of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA binding molecule screening; inhibition of transcription; infection; human immunodeficiency virus; HIV; parasite; cancer; cardiovascular; respiratory; gastrointestinal; endocrine; metabolic; rheumatic; immunological; haematological; neurological; psychiatric; dermatological; ophthalmological; musculo-skeletal; urogenital disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 21.4; DB 20; Length 4
Pred. No. 5.8e+04;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA binding molecule screening method test sequence #156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1641 GCGGCTGGAGGGATGCCACACCCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GCGGTGGATTGGACGCTCCACCAATCACAGGGCAGCGCC 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 46 BP; 9 A; 14 C; 16 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cantor CR, Andrews BM,
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Best Local Similarity 71.8%;
Matches 28; Conservative 0
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91US-0723618.
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17-SEP-1993;
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27 - JUN - 1991
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Query Match
88888888888888
                                            The invention relates to a method of decreasing transcriptional activity in a duplex decxyribonucleic acid (DNA) template (T1) comprising contacting (T1) with a binding agent comprising at least one small duplex binding molecule (T2) coupled to at least one other small duplex. DNA-binding molecule that binds to a non-overlapping region of target franscription of a sequence (TS). The method is useful for inhibiting transcription of a range of disease-related genes for treating infections (by viruses, not cluding human immunodeficiency virus, bacteria, fungi, protozon and parasites), cancer, cardiovascular, respiratory, gastrointestinal, and parasites), cancer, cardiovascular, respiratory, gastrointestinal, cancolorial, parasites, parallatic, dermaticional, hemmaticional, nemaciological, menschogical, penetic urogenital discretes. The method provides sequence-specific inhibition of transcription of pathological genes transcription factor, and can be applied to regulated by the same ABK81492-ABK83155 represent DNA binding molecule test sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequences AAH62100 - AAH62688 represent segments of human genes which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid segments of the human genome, particularly from genes including polymorphic sites, for phenotype correlation, forensics, paternity testing, medicine and genetic analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single nucleotide polymorphism; SNP; human; cancer; inflammation; heart disease; paternity testing; forensic science; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag- a
/standard_name- 'single nucleotide polymorphism'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.2%; Score 21.4; DB 24; Length 46; larity 71.8%; Pred. No. 5.8e+04; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCTAIRE-1 polymorphism containing DNA fragment #96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1641 GCGGCTGGAGGGATGCCACACCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GCGGTGGATTGGACGCTCCACCAATCACAGGCAGCGCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46 BP; 9 A; 14 C; 16 G; 7 T; 0 other;
  Example 15; SEG ID No 156; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualiflers
replace(11,6)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH62195 standard; DNA; 21 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-2000; 2000WO-US31639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0167334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 37; 80pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200138576-A2
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Variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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contain single nucleotide polymorphisms (SNPs). A method is included in the invention for analysing a nucleic acid sample, which consists of determining the base occupying any one of the polymorphic sites given the SNP containing sequences. The nucleotide sequences can be used in the diagnosis or monitoring of diseases, such as cancer, inflammation, heart diseases, diseases of the cardiovascular system, and infection by microorganisms. The oligonocleotides are also useful in the manufacture of a medicament for the treatment or prophylaxis of the diseases, and as a pharmaceutical. SNP containing oligonucleotides are useful in medicine and genetic analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer
                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                             Length 21;
                                                                                                                                                                                                                                                                      1.2%; Score 21; DB 22; Length 21, 100.0%; Pred. No. 5.4e+04; Pred. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cervical cancer marker nucleic acid 1933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46 BP; 7 A; 13 C; 18 G; 6 T; 2 other;
                                                                                                                                                                                                                                 Sequence 21 BP; 9 A; 4 C; 6 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berger A, Zhao X;
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                                                                                                                                                                                                                                                                                                                                                702 CAAGGAGATCAGACTGGAACA 722
                                                                                                                                                                                                                                                                                                                                                                        1 CAAGGAGATCAGACTGGAACA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
AAH70659/c
ID AAH70659 standard; cDNA; 46 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2000; 2000US-0189315
12-MAX-2000; 2000US-0203791
09-JUN-2000; 2000US-0210600
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                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-375006/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200142467-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUN-2001.
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1.2%; Score 21; DB 22;

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                       Gaps
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                     Indels
Best Local Similarity 71.1%; Pred. No. 7.3e+04; Matches 27; Conservative 0; Mismatches 11;
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550 AAGCCCTCAGCGGCGCCTCCGTCGTCTCAGCCTATC 587 a ò

RESULT 15 AAL34286/c ID AAL34286 standard; DNA; 50 BP.

AAL34286;

24-JAN-2002 (first entry)

Human SNP oligonucleotide #7494

Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoletin; appotosis related protein; canherin; complement polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinase; colony stimulating factor; interleukin; G-protein coupled receptor; thhoesterase; intlammation; neuvous system disease; autoimmune disease; infection;

Homo sapiens.

W0200147944-A2.

05-JUL-2001

28-DEC-2000; 2000WO-US35498.

28-DEC-1999; 99US-0173419. 27-DEC-2000; 2000US-0173419.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2001-465210/50.

Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -

Claim 1; Page 3547; 4143pp; English

The present invention relates to oligonuclectides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopotetin, operates related proteins, cadherin, cyclin, polymerase, oncogenes, listones, kinases, colony stimulating factors. Complement related proteins, cytochromes, kinesins, cytokines, interferons, interletkins, cytokines, complement related proteins, cytochromes, kinesins, cytokines, interferons, interletkins, cytokines, complement related proteins and thioesterases. The present sequence is one such oligonucleotides and the preptides encoded by them may be used in the prevention, diagnosis and treatment of deseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune of diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus and Grave's diseases), inflammation, cancer (e.g. cancers of the bladder, breast, colon and kidney, content and an infection of pathogenic

Sequence 50 BP; 1 Å; 27 C; 11 G; 11 T; 0 other;

. ö Gaps ö 1.2%; Score 21; DB 22; Length 50; larity 66.7%; Pred. No. 7.6e+04; Conservative 0; Mismatches 15; Indels Local Similarity nes 30; Conserva Query Match

å 8

Search completed: March 3, 2003, 22:46:23 Job time : 431 secs

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Sequence 5, Application US/08334177

Sequence 5, Application US/08334177

Sequence 5, Application US/08334177

Patent No. 5696008

APPLICANT: Avraham, Hava Karsenty

APPLICANT: Godwaki, Paul J.

TITLE OF INVENTION: Methods and Kits Using Macrophage Stimulating Protein

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS: 16

CORRESPONDENCE ADDRESS: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: Galifornia

COUNTRY: USA
                                 Sequence 19, Sequence 582, Sequence 582, Sequence 582, Sequence 582, Sequence 11, Sequence 11, Sequence 5, A Sequence 5, A Sequence 5, A Sequence 6, A Seque
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
CONPUTER READABLE FORM:
NEDIGN TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: RC-DOS/MS-DOS
SOFTWARE: PALIO (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,177
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
RILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
Query Natch
1.3%; Score 22.2; DB 1;
Best Local Similarity 69.8%; Pred. No. 5.8e+03;
Matches 30; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                              US-08-683-2628-32
US-08-555-268A-5
US-08-555-268A-6
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TELEKX: 415/925-9811
TELEK: 910/371-7168
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 47 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
      ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-334-177-5
à
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Sequence 5, Appl1
Sequence 9, Appl
Sequence 156, Appl
                                                                                                                                                                    March 3, 2003, 22:35:55; Search time 76 Seconds (without alignments) 7041.460 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                        1 tggaagcagcgtaaaggatg......gttcacctgcccacttgtcc 1745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/lna/5A_COMB.seq:*
/cgn2_6/ptodata/1/lna/5B_COMB.seq:*
/cgn2_6/ptodata/1/lna/6A_COMB.seq:*
/cgn2_6/ptodata/1/lna/6B_COMB.seq:*
/cgn2_6/ptodata/1/lna/PtoTG2_COMB.seq:*
/cgn2_6/ptodata/1/lna/PtoTG2_COMB.seq:*
               GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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05-08-129-36-156
05-08-475-2288-156
05-08-482-080A-156
PCS-09-39-47-156
PCS-09-33-009-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-414-117-47
-09-678-437-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441362 seqs, 153338381 residues
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                                                                                                                nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                 US-10-017-621-3
1745
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19.
                                                                                                                   OM nucleic
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Result

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) OTHER INFORMATION: Description of Artificial Sequence:Synthetic contern INFORMATION: ribozymes and portions thereof US-08-507-426c-9
                                                                                                                                 Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Turin, Lisa M.
APPLICANT: Furner B.
APPLICANT: Turin, Compositions and Methods NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEDE: Genelabs Technologies, Inc.
                                                                                                                                                                                                                                        1559 CGTCGATGCCTGACTCAGGCAGGCCAGCTTTCCGCGTGGTG 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : INDIVIDUAL ISOLATE: Human H1 histone gene FNC16
78-08-171-389-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-OGS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
                                                                                                                                                                                                                                                                     42 CCTTGGTGGACGACTCAGGCACTCCTGCTTTGCGCCTGCTG 2
                                                                                                                                 Ouery Match 1.2%; Score 21.8; DB 4; Best Local Similarity 70.7%; Pred. No. 7.2e+03; Matches 29; Conservative 0; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Genelabs Technologies, Inc.
505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 156, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Ithear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08507426C.
Sequence 9, Application US/08507426C.
Sequence 9. Application US/08507426C.
Patent No. 6265634
Sequence 9. Application US/08507426C.
Sequence 9. Application US/08507426C.
TITLE OF INVENTION: POLYRIBOZIME CAPABLE OF CONFERRING ON PLANTS RESISTANCE: TITLE OF INVENTION: POLYRIBOZIME STITLE OF INVENTION: POLYRIBOZIME: TITLE OF INVENTION: POLYRIBOZIME: TITLE OF INVENTION: POLYRIBOZIME: TITLE OF INVENTION: POLYRIBOZIME: TO/08/507,426C.
CURRENT APPLICATION NUMBER: 43944-A-PCT-US PRIOR FILING DATE: 1995-10-25 NUMBER OF SEQ ID NOS: 14 SOFFWARE: Patentin Ver: 2.1
SEMCTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                   Sequence 5, Application PC/TUS9513830
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: New England Deaconess Hospital Corp.
TITLE OF INVENTION: Wethods and Kits Using Nacrophage Stimulating TITLE OF INVENTION: Protein NUMBER OF SEQUENCES: 10
CORRESPONDENCES: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 5.8e+03;
0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GGCGCCAGTGACCCTGGAGGCCCCCCACACGTGCTGCTG 283
2 GCACGAATCCACCATGGGGTGGCTCCCACTCCTGCTGCTTCTG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGACGAATCCACCATGGGGTGCCTCCACTCCTGCTTCTG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDLION TYPE: 3.5 inch, 1.44 Mb floppy disk
CMUDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MINDRAIN (Genentech)
CURRENT APPLICATION DATE:
APPLICATION NUMBER: PCT/US95/13830
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc.
STREET: 460 Point san Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MARSCADANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0911
TELECOMUNICATION INFORMATION:
TELEPHONE: 415/255-516
TELEFRA: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415/952-9881
TELEX: 910/371-7168
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.3%;
Best Local Similarity 69.8%;
Matches 30; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: '47 base pairs
TYPE: Nucleic Acid
GTRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-507-426C-9/c
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PCT-US95-13830-5
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ò 셤 Application US/08475228A

USA

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APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
NUMBER OF SEQUENCES: 664
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

NEDIUM TYPE: Floppy disk

COMPUTER: IBM PC comparishe

OCHRUTER: IBM PC Comparishe

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: U6-JUN-1995

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: U5 08/123,936
                                                                                                                                                                                                                                    NUMBER OF SEGUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 05 08/123,936
FILING DATE: 17.5EP-1993
RILING DATE: 17.5EP-1993
APPLICATION DATA: 05 07/996,783
FILING DATE: 23.0EC-1992
PHIOR APPLICATION DATA: 07/723,618
FILING DATE: 27.0UN-1991
PRIOR APPLICATION DATA: 07/723,618
FILING DATE: 27.0UN-1991
PRIOR APPLICATION DATA: 05 08/081,070
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
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                                                        Gaps
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            Length 46;
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                                                                                                                                                                                                                                                                                                    APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of YOMBER OF SEQUENCES: 640
CORRESPONDENCE: 640
    Score 21.4; DB 1; Length 4 Pred. No. 9.3e+03; 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; INDIVIDUAL ISOLATE: Human H1 histone gene FNC16 US-08-123-936-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN RELEASE #1.0, Version #1.25
CURENT APPLICATION DARM:
APPLICATION NUMBER: US/OB/123,936
                                                                                   1641 GCGGCTGGAGGGATGCCACACCCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1641 GCGGCTGGAGGGATGCCACACCCCTCACAGGGCAGCCCC 1679
                                                                                                                   2 GCGGTGGATTGGACGCTCCACCAATCACAGGGCAGCGCC 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,875
REGISTRATION NUMBER: 4600-0075.32/G19P2
TELECHNUNICATION HUMBER: (460-0075.32/G19P2
TELEPHONE: (415) 324-0980
TELEFAX: (415) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: Genelabs Technologies, Inc.: 505 Penobscot Drive
Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                              Sequence 156, Application US/08123936
Patent No. 5726014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
Query Match 1.2%;
Best Local Similarity 71.8%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 324-0960
ORMATION FOR SEO ID NO: 1
EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.28
Best Local Similarity 71.88
Natches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94063
COMPUTER READABLE FORM:
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EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE
                                                                                                                                                                                                                     -123-936-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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Length 46;
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US-08-475-228A-156
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APPLICATION NUMBER: US 08/081,070
PILICATION NUMBER: US 08/081,070
PILICO DATE: 22-JUN-1993
ATOCNEY/ACENT INFORMATION:
NAME: Stratford, Carol A.
RECIENTATION NUMBER: 44,44
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.2%; Score 21.4; DB 2; Best Local Similarity 71.8%; Pred. No. 9.3e+03; Matches 28; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GCGGTGGATTGGACGCTCCACCATCACAGGGCAGCGCC 40
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Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                  LENGTH: 46 base pairs
                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL:
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APPLICANT: Turin, Lisa M.
APPLICANT: Fur, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
STREET: 505 Penobscot Drive
STREET: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO SPECIAL SOURCE: CANDIVIDUAL ISOLATE: Human H1 histone gene FNC16 US-09-354-347-156
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DAIA:
FILING DAFE: US/09/354,947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1641 GCGCTGGAGGCATGCCACACCCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4600-0175.20/G19P3D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.2%; Score 21.4; DB 4; Best Local Similarity 71.8%; Prad. No. 9.3e+03; Matches 28; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GCGTGGATTGGACGCTCCACCAATCACAGGGCAGCGCC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,080
FILING DATE: 07-001-1995
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                      COUNTRY.

ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TTPE: Floppy disk
MEDIUM TTPE: Floppy disk
"WETTER: IBM PC COMPALIBLE
"WETTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/996,783 FILING DATE: 23-DEC-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/723,618 FILING DATE: 27-20N-1991 PRIOR APPLICATION DATA: US 08/081,070 APPLICATION NUMBER: US 08/081,070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/081,070 FILING DATE: 22-JUN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BEADY, JOHN F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0860
TELEPAR: (650) 324-0960
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear NOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                               CITY: 1
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            å
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                                                                 APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Wolecules, Compositions and Methods
UNMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                            WEDUTURY TYPE: Floppy disk
COMPUTER: INH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Roless
FILING DATE: 07.-JUN-1995
RILING DATE: 20-DEC-1993
RILING DATE: 20-DEC-1993
RILING DATE: 17-SEP-1993
RILING DATE: 17-SEP-1993
RILING DATE: 23-DEC-1992
PRICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
RILING DATE: 23-DUN-1991
RILING DATE: 22-JUN-1993
ATTORNEY AGENT INFORMATION:
NAME: MARCH INDAGENT INFORMATION:
NAME: ARACL TANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: Human H1 histone gene FNC16
US-08-482-080A-156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1641 GCGCTGGAGGGATGCCACACCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/COCKET NUMBER: 4600-0175.20/G19P3D1
FELECOMUNICATION INFORMATION:
TELEPHONE: (650) 124-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GCGGTGGATTGGACGCTCCAATCACAGGGCAGCGCC 40
                                                                                                                                                                            SEE: Gendlabs Technologies, Inc.: 505 Penobscot Drive
Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 156: SEQUENCE CHARACTERISTICS: LENGTH: 46 base pairs TYPE: nucleic acid
Cantor, Charles R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                          Beth M.
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                                                                                                                                                                                                                                                                                                                          OMPUTER READABLE FORM:
NEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                COUNTRY:
                  APPLICANT:
APPLICANT:
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Sequence-Directed DNA Binding
Molecules, Compositions and Methods
641
                              Sequence 156, Application PC/TUS9312388 GENERAL INFORMATION:
                                                                 APPLICANT:
TITLE OF INVENTION: S
TITLE OF INVENTION: M
RESULT 9
PCT-US93-12388-156
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Sequence 156, Application US/09354947 Patent No. 6384208

RESULT 8 US-09-354-947-156

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GENERAL INFORMATION:
APPLICANT: BEWARDS, CYNTHIA A.
APPLICANT: CANLOT, Charles R.
APPLICANT: ANDIEWS, BELD M.

Gaps

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TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ANTI-SENSE: YES
US-08-233-009-33
                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-08-285-936-38/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
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APPLICANT: Jacobson, Robert G
APPLICANT: Johnson, Robert G
APPLICANT: Salvatore, Christopher A
TITLE OF INVENTION: INHIBITION OF EDSINOPHIL
TITLE OF INVENTION: ACTIVATION THROUGH A3 ADENOSINE RECEPTOR ANTAGONISM
NUMBERS OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STRRET: P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.2%; Score 21.4; DB 5; Length 46; Best Local Similarity 71.8%; Pred. No. 9.3e+03; Matches 28; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Fablan, Gary R.
REGISTRATION NUMBER: 33,675
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
FELECOMUNICATION INFORMATION:
FELECOMONICATION INFORMATION:
FELERAX: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 156:
SEQUENCE CHRACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                            COMPTER REPABLE FORM:
WEDING TYPE: Floppy disk
WEDING TYPE: IBM FC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; INDIVIDUAL ISOLATE: Human H1 histone gene FNC16 PCT-US93-12388-156
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WEDIUM TYPE: Floppy disk
COMPUTER: IBH PC compatible
COMPUTER: IBH PC compatible
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1641 GCGCTGGAGGGATGCCACACCCCTCACAGGGCAGCCCC 1679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GCGGTGGATTGGACGCTCCAATCACAGGGCAGCGCC 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33, Application US/08233009
Patent No. 5646156
GEMERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New Jersey
COUNTRY: United States
21P: 07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                           CILL.
STATE: CA
COUNTRY: USA
'D. 94063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rahway
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FILING DATE: 25-APR-1994

ATOMESTICATION WHORER: 109/08/233,009

FILING DATE: 25-APR-1994

ATOMESTICATION WHORE: 32-APR-1994

ATOMESTICATION WHORE: 32-APR-1994

FILING DATE: 35-APR-1994

FORGER DATE:
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INHIBITORY/INSTABILITY REGIONS OF MRNA
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INHIBITORY/INSTABILITY REGIONS OF MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 GAGATTGTGCACGAGGACTTGAAGATGGGGTCTGATGG 362
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TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY
NUMBER OF SEQUENCES: 130
NUMBER OF SEQUENCES: 130
SOURESSEDE: MORGEN & FINNEGAN
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-00-50-478-47
Sequence 47, Application US/08050478
Patent No. 5972596
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: INHIBITORY/IN
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN
STRET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA YORK
ZIP: 10154
COMPUTER REALABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM
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STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: LINEAR
US-08-850-049-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Velton, Dale
APPLICANT: Velton, Dale
APPLICANT: Velton, Dale
APPLICANT: Nosov, William
APPLICANT: Huse, William
APPLICANT: Rosov, William
APPLICANT: Rosov, Wase J.
TITLE OF INVERTION: No. 5792456el Mutant BR96 Antibodies and
TITLE OF INVERTION: Functional Equivalents Reactive With Human Carcinomas
CORRESPONDENCES: 62
CORRESPONDENCES
                                                                               Query Match
1.24; Score 20.6; DB 1; Length 45;
Best Local Similarity 67.44; Pred. No. 1.56+04.
Matches 29; Conservative 0; Mismatches 14; Indels
Matches 29; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 1.20; Score 20.6; UB 1; Length 45; Best Local Similarity 67.44; Pred. No. 158+04. Matches 29; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTEY: UGA
COMPUTEY: UGA
COMPUTEY: UGA
COMPUTER: RELORDY disk
MEDIOM TTPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTES: IBM PC compatible
COMPUTED: PREDITOR SIGNER: US/08/487,860
FILING DATE: UT-UN 1995
CLASSIFICATION: S10
ATORNEY/AGENT INFORMATION:
NAME: Adilano, Sarah B.
RECERRICE/DOCKET NUMBER: 34,470
RECERRICE/DOCKET NUMBER: 34,470
RECERRICE/DOCKET NUMBER: 34,470
RECERRICE/DOCKET NUMBER: 310-445-1140
TELEPHONE: 310-445-9031
INFORMATION FOR SED ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TEMPOTALION FOR SED ID NO: 38:
TEMPOTALION FOR SED ID 
                                                                                                                                                                                                                                          328 ATTGTGCACGAGGACTTGAAGATGGGGTCTGATGGGGAGAGTG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328, ATTGTGCACGAGACTTGAAGATGGGGTCTGATGGGGAGAGTG 370
                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-06487-860-38/c
; Sequence 38, Application US/08487860
; Patent No. 5792456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47, Application US/08850049;
Patent No. 5965726
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (genomic) US-08-487-860-38
    US-08-285-936-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-850-049-47
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us-10-017-621-3.lim50.rni

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Query Match 1.2%; Score 20.4; DB 4; Length 48; Best Local Similarity 71.1%; Pred. No. 1.7e+64; Matches 27; Conservative 0; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/958,747
FILING DATE: 27-MAR-1992
CLASSIFICATION:
ATTONNEY FACRET INFORMATION:
NAME: MORRY, MARK J.
REGISTRATION NUMBER: 34,398
REFERENCE/POCKET NUMBER: 2026-4006US1
TELECONUMICATION INFORMATION:
TELECONUMICATION INFORMATION:
TELECONUMICATION INFORMATION:
TELECONUMICATION INFORMATION:
TELECONUMICATION INFORMATION:
TELECONUMICATION INFORMATION:
TELECONUMICATION OF SEQ 10 NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SIGGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: March 4, 2003, 00:52:00 Job time : 80 secs
                                            29-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: LINEAR
US-09-414-117-47
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APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILLITY REGIONS OF MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.2%; Score 20.4; DB 2; Length 46; Best Local Similarity 71.1%; Pred. No. 1.7e+04; Matches 27; Conservative 0; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 GACACGCTGCCCTGAACTTGAAGCCGGGGATGGATGG 44
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IAM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/958,747
FILING DATE: 27-MAR-1992
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: WORRY, MARY J.
RECISTRATION NUMBER: 24,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION PROPREMATION:
TELECOMMUNICATION PROPREMATION PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCI/US93/02908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/414,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-03-414-117-47
Sequence 47, Application US/09414117; Patent No. 6291664
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/650,049
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: FLORPY DISK COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: SINCLE
TOPOLOGY: LINEAR
US-08-050-478-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
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March 3, 2003, 22:39:05; Search time 133 Seconds (without alignments) 8182.066 Million cell updates/sec
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1745
1 tggaagcagcgtaaaggatg.....gttcacctgcccacttgtcc 1745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications NR:*

1: \cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: \cgn3_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

3: \cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

4: \cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: \cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

6: \cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

7: \cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

8: \cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: \cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

10: \cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

10: \cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: \cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

12: \cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

13: \cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

14: \cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*

14: \cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254638
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460893 seqs, 311809382 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0 Maximum DB seq length: 50
                                                                                                                                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 107, App Sequence 1339, A Sequence 1313, Ap Sequence 18, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 21, Appl Sequence 2, Appl Sequence 16, Appl Sequence 16, Appl Sequence 226, Appl Sequence 226, Appl Sequence 226, Appl Sequence 226, Appl Sequence 226, Appl Sequence 24, Appl Sequence 25, Appl Sequence 26, Appl Sequence 27, Appl Sequence 26, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 26, Appl Sequence 27, Appl Sequence 21, Appl Sequence 31, Appl Sequence 311, Ap	Fel dI, Expressed in and Treatment of Cat Allergy NUMBER: 09/410,963	ength 48; Indels 0; Gaps 0; 2
US-09-840-277-107 US-09-866-108-15395 US-09-864-785-3433 US-09-938-48-78-3433 US-09-781-534A-18 US-10-129-248-31 US-09-9343-722-31 US-09-9343-722-31 US-09-9343-722-31 US-09-9343-722-31 US-09-9343-722-31 US-09-9343-722-31 US-10-036-314-8 US-10-036-314-8 US-10-036-314-16 US-10-036-314-16 US-10-036-314-16 US-10-036-314-16 US-10-036-314-16 US-10-036-314-16 US-10-073-356-34 US-10-073-356-34 US-10-073-356-34 US-10-073-256-33 US-09-864-785-3267 US-09-864-785-3367 US-09-864-785-3367	tergen, lergen, lagnosis la4 (CATION.: 1999-1	21.8; DB 9; L No. 9.5e+03; matches 12; CAGAACCIGCIC 100 [
974448888844444488444444444444444444444	RESULT 1 Sequence 6, Application US/10054444 Sequence 6, Application Namen Cat All TITLE OF INVENTION: Beculovitus for DI FILLS OF INVENTION: Beculovitus for DI FILLS OF INVENTION: Beculovitus for DI FILLS FREERENCE: DC-0118 CURRENT APPLICATION NUMBER: US/10/054, CURRENT FILING DATE: 2002-01-22 PRIOR APPLICATION NUMBER: EARLIER APPLISTON FILING DATE: NUMBER OF SEQ 1D NOS: 6 SOFTWARE: Patentin Ver. 2.0 SEQ 1D NO 6 LENGTH: 48 TYPE: DNA ORGANISM: Artificial Sequence FRATURE: CONTRACT OF ACT OF	Query Match Best Local Similarity 70.74; Pred Best Local Similarity 70.74; Pred Matches 29; Conservative 0; Mi 962 AGAAGGTGCTACACGCCGAGACCTCAAGCCC
	6 Applicat S200201 SPATION SPATION SPATION NO. 21 GOLGSTE NO. 21 NO. 21 SPATION SPATION SPATION ACTIFICIA	Similarity 70. Similarity 70. Conservative AGGTGCTACACCGAGA ACCTCCTCCACCAGAA -752 -752 -752 Cargill, Michele Gargill, Michele Ireland, James
100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ULT 1 Guence 6, Applicatio Tent No. US200201643 Guence 6, Applicatio Tent No. US200201643 PPLICANT GUASALINON: PPLICANT: GUASCELIN PPLICANT: GUASCELIN PPLICANT: GUASCELIN PPLICANT: GUASCELIN PPLICANT: GUASCELIN PPLICATION: TILE OF INVENTION: R TILE OF INVENTION: R TILE OF INVENTION: R TILE OF INVENTION OF TILE OF INVENTION OF TILE OF INVENTION OF TILE OF INVENTION OF THE INTERIOR FILING DATE: EA THE FILING DATE: EA THE INTO FILING NATE THE INTO	Query Match Best Local S Matches 29 Matches 29 Matches 29 1111 2 AGAA 2 109-801-274- SSULT 2 3 09-801-274- Sepance 752 Patch No. U GENERAL INFO APPLICANT:
0 0 00 0000 0000 0000 0000 0000 0000 0000	RESOLT US-10- Sequence of the part of the	Overy Overy Overy Overy Overy Overy Over Over Over Over Over Over Over Over

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TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF MRNA
NUMBER OF SEQUENCES:
ADDRESSONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                         Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.2%; Score 21; DB 10; Best Local Similarity 77.4%; Pred. No. 1.34-104; Matches 47; Conservative 1; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION UNMER: US 07/856,747
FILING DATE: 27-MAR-1992
CLASSIFICATION:
ATORNEY-AGENT INFORMATION:
NAME: MORKY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET UNMER: 2026-4006US1
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)759-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      577 GECAGCCIATCTGAGATTGGCTTTGGGAAAC 607
    PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SCPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 94
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: DSA

COMPUTER READABLE FORM:
MEDIUM TYERS: FLORPY DISK
COMPUTER: TRAN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
RPLICE DATE:
FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/850,049
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: PCT/US93/02908
29-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S-09-943-722-47
Sequence 47, Application US/09943722
Publication No. US20020192660A1
GENERAL INFORMATION:
APPLICANT:
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INPORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGIH: 48 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: P
FILING DATE: 29-MAR-1
CLASSIFICATION:
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TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo saplens
US-09-801-274-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Malouf, Nadia
APPLICANT: Michols, Timothy C.
TITLE OF INVENTION: Purified and Isolated Platelet Calcium Channel Nucleic Acids and
TITLE OF INVENTION: Polypeptides and Therapeutic and Screening Methods Using Same
FILE REFERENCE: 421/29
CURRENT APPLICATION NUMBER: US/10/029,413A
CURRENT FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 31;
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLECTIDE POLYMORPHISMS: FILE REFERENCE: 2825.2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT APLICATION NUMBER: US 60/187,510
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ 10 NOS: 1802
SOCTHARE: EastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 1.24; Score 21.4; DB 9; Length 45; Best Local Similarity 80.64; Pred. No. 1.2e+04; Matches 25; Conservative 0; Mismatches 6; Indels
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Perfent No. US2002032319A1
PERFENT INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Ireland, James S.
APPLICANT: Lender, Eric S.
FILE REFRENCE: 2825,2009-001
CORRENT APPLICATION NUMBER: US/09/801.274
CURRENT APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 1.2%; Score 21.6; DB 10;
Best Local Similarity 80.0%; Pred. No. 8.8e+03;
Natches 24; Conservative 1; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GACATCAAGCCCCAKAACCTGCTGGTGGAC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-029-413A-25
; Sequence 35, Application US/10029413A
; Patent No. US20020165353A1
- GRMERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
GRGANISM: Homo sapiens
US-09-801-274-752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HANE/KET: partial_cDNA (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45) (1)...(45)
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
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, TOPOLOGY; US-09-943-722-47

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us-10-017-621-3.1im50.rnpb

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APPLICANT: Hood, Leroy E.
APPLICANT: Roven, Lee
APPLICANT: Roven, Lee
APPLICANT: Roven, Lee
TITLE OF INVENTION BIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND NETHODS WHICH UNTERSPONDENCE ADDRESS: 1279
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                               Gaps
            FEATURE:
GOTHER INFORMATION: Description of Artificial Sequence: synthetic
COTHER INFORMATION: oligonucleotide used to insert codon between VH
COTHER INFORMATION: and VL domains of NCIO scFv-0
US-09-147-142-12
                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 40;
                                                                                                                                                                                                                                               Length 45;
                                                                                                                                                                                                                                  Query Watch 1.1%; Score 20; DB 10; Length 45
Best Local Similarity 65.9%; Pred. No. 2.8e+04;
Matches 29; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                     643 GGTACCTATGCCACCGTCTACAAAGGCAAAAGCAAGCTCACAGA 586
                                                                                                                                                                                                                                                                                                                                                                                                                                        45 GGGACCACGGTCACCGTGGTGATATCGAGCTCACACA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MELLON TIES.
COMPACTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-NAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19.8; DB 10;
Pred. No. 3c+04;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1689 CTTCCCTGCTTACTCTGCCTACCTGCCTG 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CTTCCTTCTTTCCTTCTTCTTCCTGCCTG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-09-790-417-235/c
: Sequence 235, Application US/09790417
: Patent No. US20010031470A1
: GENERAL INFORMATION:
: APPLICANT: Shultz, John W
: APPLICANT: Lewis, Martin K.
: APPLICANT: Lewis, Martin K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 758, Application US/09263959
Patent No. US20020150891A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNET/AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.1%;
Bost Local Similarity 77.4%;
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY; linear
US-09-263-959-758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HUDGON, Peter John
APPLICANT: KORTT, Alex Andrew
APPLICANT: KORTT, Alex Andrew
APPLICANT: RONGT, Alex Andrew
APPLICANT: RYNELG, Alexander
APPLICANT: AFFELG. JOHN LESSIG
TITLE OF INVENTION: HIGH AVIDITY POLYVALENT AND POLYSPECIFIC REAGENTS
CURRENT APPLICATION WUMBER: US/09/147,142
CURRENT FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: PCT/AU98/00212
BARLIER APPLICATION NUMBER: AU PO 5917
WHARD COLOR CO
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APPLICANT: KORTT, Alex Andrew
APPLICANT: KORTT, Alex Andrew
APPLICANT: INVING, Robert Alexander
APPLICANT: ATWELL, John Leslie
FILLE OF INVENTION: HIGH AVIDITY POLYVALENT AND POLYSPECIFIC REAGENTS
FILE REFERENCE: 0167086/0212
CURRENT APPLICATION NUMBER: US/09/147,142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: synthetic profile InFORMATION: oligonucleotide used to insert codon between VH OTHER INFORMATION: and VL domains of NCIO scFv-0 US-09-147-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                    Query Match 1:2%; Score 20.4; DB 9; Length 48; Best Local Similarity 71:1%; Pred. No. 2:38+04; Matches 27; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      643 GGTACCTATGCCACCGTCTACAAAGGCAAAAGCAAGCTCACAGA 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGGACCACGGTCACCGGTGGTGATATCGAGCTCACACA 44
                                                                                                                                                                                                                                                   325 GAGATIGTGCACGAGGACTTGAAGATGGGGTCTGATGG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.1%; Score 20; DB 10;
Best Local Similarity 65.9%; Pred. No. 2.8e+04;
Matches 29; Conservative 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                          7 GAGACGGTGCCCGTGAAGTTGAAGCCGGGGATGGATGG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: PCT/AU98/00212
EARLIER FILING DATE: 1998-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: AU PO 5917
EARLIER FILLING DATE: 1997-03-27
SOFTWARE: PETENTIN VOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 11, Application US/09147142
; Patent No. US20020018749A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09147142
Patent No. US20020018749A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
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LINEAR
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-09-147-142-12/c

ò g TYPE: DNA

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Sequence 111, Application US/09263959
Petert No. U350020150891A1
Petert No. U350020150891A1
Petert No. U350020150891A1
APPLICANT: ROWEN, Lee
APPLICANT: ROWEN, Lee
APPLICANT: ROWEN, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UNUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.1%; Score 19.2; DB 10; Length 31; Best Local Similarity 80.8%; Pred. No. 3.9e+04; Matches 21; Conservative 1; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                     Query Match 1.1%; Score 19.4; DB 12; Length 45; Best Local Similarity 64.4%; Pred. No. 4.1e+04; Matches 29; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CACALLIA, Michele
APPLICANT: Ireland, James S.
APPLICANT: Ireland, James S.
APPLICANT: Ireland, James S.
APPLICANT: Lander, Elic S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REPRENEE: 2825, 2009-001
CURRENT APPLICATION NUMBER: US/09/801, 274
CURRENT PILING DATE: 2001-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEO ID NOS: 1802
SOFTWARE: FastSEO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                            1288 ATCCTGTCCAACGAGGAGTTCAAGACATACAACTACCCCAAGTAC 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
FILE REFERENCE: 19124.0002
CURRENT APPLICATION NUMBER: US/10/073,256
CURRENT FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1190 CCACAGGCCGTCCCTTTTCCGGGC 1215
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Sequence 517, Application US/09801274

Patent No. US20020032319A1

GENERAL INFORMATION:
                                                                                                                                                                                                          TYPE: DNA
CRGANISM: Enterococcus faecalis
US-10-073-256-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo saplens
US-09-801-274-517
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STATE: Washingt
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-09-263-959-121/c
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US-10-01-256-27/C
Sequence 27, Application US/10073256
Petent No. US/2002104008A1
PETENT US/2002104008A1
APPLICANT: Kreiswirth, Barry N
APPLICANT: Reliavirth, Barry N
APPLICANT: Reliavirth, Barry N
APPLICANT: Reliavirth, Barry N
APPLICANT: Reliavirth, Barry N
APPLICANT: Model, Steven M
TITLE OF INVERTIONS: System and Method for Tracking and Controlling Infections
FILE REPRENCE: 1914.0002
CURRENT APPLICATION NUMBER: US/10/073,256
CURRENT FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35, Application US/10073256
Patent No. US2002012040BA1
GENERAL INFORMATION:
APPLICANT: Kreiswirth, Barry N
APPLICANT: Nadich, Steven M
TILE OF INVENTION: System and Method for Tracking and Controlling Infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:probe for oligo; OTHER INFORMATION: 54
US-09-790-417-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.14; Score 19.6; DB 10; Length 42; Best Local Similarity 66.74; Pred No. 3.5e.40; Matches 28; Conservative 0; Mismatches 14; Indels Watches 28; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 1.14; Score 19.4; DB 12; Length 45; Best Local Similarity 64.44; Pred. No. 4.1e+04; Matches 29; Conservative 0; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 GTACCTGGTAAATGAACTCACCCACGATATCATCACCAAGCT 1
                                                                                                                          APPLICANT: Gu, Trent
APPLICANT: Gu, Trent
APPLICANT: Glson, Ryan J.
APPLICANT: Wood, Keith W.
APPLICANT: Wood, Keith W.
APPLICANT: Wood, Keith W.
TITLE OF INVENTION: Nucleic Acid Detection
FILE REFERENCE: Pro-103 6686/75528
FILE REFERENCE: POOL-02-22
FRICH PAPLICATION NUMBER: 09/389,972
PRICH PLILKE DATE: 1999-07-21
PRICH PLILKE DATE: 1999-07-21
PRICH PLILKE DATE: 1999-07-21
PRICH PLILKE DATE: 1999-03-13
SOFTWARE: PALENTIN NUMBER: 09/042,287
PRICH FLILKE DATE: 1999-03-13
SOFTWARE: PALENTIN VEY: 2.0
SEQ ID NO 235
LENGH: 42
                            Kephart, Daniel
Rhodes, Richard B.
Andrews, Christine A.
Hartnett, James R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Enterococcus faecalls
US-10-073-256-27
   Mandrekar, Michelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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US-10-073-256-35/c
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Search completed: Narch 4, 2003, 00:54:25
Job time: 134 secs
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APPLICANT: Santino, Colleen G
APPLICANT: Santino, Colleen G
TITLE OF INVENTION: No. 08200120192813Alel Plant Expression Vectors
FILE REFERENCE: monocot elements
CURRENT APPLICATION NUMBER: US/09/376,940A
CURRENT FILING DATE: 1999-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence:synthetic US-09-376-940-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.1%; Score 19; DB 9; Length 43; Best Local Similarity 65.1%; Pred. No. 5.1e+04; Matches 28; Conservative 0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 GTGTCCACCCCTCGATCTCTCGCTCGCCCCCCCGCGATCG 1
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
PPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19.2; DB 10
Pred. No. 4.7e+04;
0; Mismatches B
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TITLE OF INVENTION: HERADNAVIRUS RECEPTOR
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 GCACCAGAGATTGTGCACGAGGACTTGAAGAT 350
                                                                                                                                   CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFENCE/COCKET NUMBER: 920010.426C2
TELECOMMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 GCACCAGAGTTTCTGCACAGGGGGGGGAGT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 60/097150
EARLIER PILING DATE: 1998-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/09376940A Publication No. US20020192813A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/09818066 Patent No. US20020032307A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FON SEQ ID NO: 123
SEQUENCE CHRARATERISTICS:
LENGTH: 46 base poirs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.1%;
Best Local Similarity 75.0%;
Matches 24; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY;
US-09-263-959-121
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                  NAME: Fraser, Janis K.
REGISTRATION NUMBER: 31,819
REFERENCE/DOCKET NUMBER: 00786/287002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1343 CCCTTTTGAGCCACGCACCCCGACTTGATAGCGAC 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CCCTTTTGAGCCACGAATTCCAGGATGAAACAGAC 36
                                                                                                                               APPLICATION NUMBER: US/09/818,066
FILING DATE: 27-Mar-2001
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/683,262
FILING DATE: 18-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-818-066-32
                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 200154
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.41
Matches 25; Conservative
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AU105237 AU105237 BM293711 S009-0-35 AZ311362 1M0026F16 AU106960 AU106960 AZ31136 1M0059H04 AZ31536 1M0059H04 AZ31536 1M0059H04 AZ985975 SU0268F01 AZ04601 MU25C05.r

HHBI1451 SALK OSSE WA3000 & 20246881 AU104829 AU104829 BG422154 60244881 AU103357 AU103357 AU103358 AU103358 AU103358 AU103358 AU103358 AU103381 AU103358 AU103381 AU103318 AU103381 AU103318 AU103381 AU103318 AU10381 AU10332 AU10323 AU10332 AU103381 AU10332 AU10333 AU10332 AU10333 AU1033583 AU103583 AU103363 AU103583 AU103363 AU103583 AU103363 AU103583 AU103383 AU103583 AU103383 AU103583 AU103383 AU103583 AU103383 AU103583

Title: Perfect score: Sequence:

nucleic

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Run 중

Scoring table:

Searched:

Database

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E Homo saplens
Eutheria: Primates; Craniata; Vertebrata; Euteleostomi;
Eutheria: Primates; Catarrhini; Hominidae; Homo.

Nammalla: Eutheria: Primates; Catarrhini; Hominidae; Homo.

Hillater, L. Lennon, G., Becker, M., Bonaldo, M.F., Chlapelli, B.,

Chissoe, S., Dietrich, N., Dibuquer, T., Pavello, A., Gish, M., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Mardis, E., Noore, M., Morriscons, J., Prange, C., Rikin, L., Rohlfing, E., Noderwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags

E 97044478
                                                                                                                                                                                                                                                                                                                                                                                                       46.bp mRNA linear EST 28-JAN-1997 yv71g05.rl Soares fetal liver spleen lNFLS Homo sapiens CDNA clone IMAGE:248216 5' similar to gb.X66363 SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1 (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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BH790015
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Fax: 31
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ACCESSION
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AU102877 AU102877
                                                       March 3, 2003, 22:34:05 ; Search time 2628 Seconds
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10753.853 Million cell updates/sec
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      GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                         - nucleic search, using sw model
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Match
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AU103382 AU103382 AU103553 AU103553 AU104162 AU104162 BI910989 603069394

est@watson.wustl.edu

Score

Š Result

45 28 23.2 21.4 21.2

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/db_xref-"taxon:9606"
/clone-"IMAGE:25073"
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                                                                                                                            Email: estévatson.wustl.edu
Insert Size: 1349
High quality sequence storts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free
through LLNL: contact the IMAGE Consortium (infoélmage.llnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 1349
Std Error: 0.00
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 26)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucabo, T., Le, M., Lennon, G., Marra, M., Parsons, J., M., Milliamson, M., Rohldmann, P. and Wilson, R.

R., Williamson, A., Rohldmann, P. and Wilson, R.

The Wash Unexek Est Project
Unpublished (1995)
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This clone is available royalty-free through LLNL; contact the INABC Consortium (info@image llnl.gov) for further information. INABC consortium (info@image llnl.gov) for further information. Insert Length: 1438 Std Error: 0.00 Seq primer: reverse ET High quality sequence stop: 1. Location/Qualifiers
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H444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.6%; Score 45; DB 14; Length 46; Best Local Similarity 97.8%; Pred. No. 0.78; Matches 45; Conservative 0; Mismatches 1; Indels
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High quality sequence stop: 1.
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/Jab_host="B."
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 306, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, OT
84112, USA
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                                                                                                                                                                   Nus musculus
Eukaryota, Werazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Werazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 36)
Euro, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Elslam, H., Longacre, S., Mahmoud, M., Meenen, E., Pederaen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
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High quality sequence stop: 36.
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HSI01159, mRNA sequence.
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1 (bases 1 to 50)
Suzukl,Y., Taira, H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata, H., Tsunoda,T., Motshima-Sugano,J., Sese,J., Hata,Y., Ota,T., Isogal,T., Tanaka,T., Motshita,S., Okubo,K., Sakaki,Y., N., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of many start sites

EMBO Rep. 2 (5), 188-193 (2001)
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukiéims.-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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/note**Organ: lung; vector: pOTB7; Site_1: XhoI; Site_2: BCORI, CDNA made by ollgo-dr prining. Directionally cloned into EcoRIX/AbI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1:8bb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).*
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1M0081COIR Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0081COI R, DNA sequence.
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/db_xref="taxon:9606"
/clone="Hsī0li59"
/note="Differential display comparison of untreated and dimethyliumarate treated U937 cells"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HRC08919"
                                                                                                                                                                                                                                                            558 CAGCCGCCCCCCCTCGTGTCAGCCTAT 586
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Local Similarity 82.8%;
hes 24; Conservative 0
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: Suzukielms.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
1. -50
                                                                            Homo sapiens
Eukaryota: Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki, Y., Paira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isagai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initation revealed by fine, large-scale mapping of mRNA start sites
ENBO REP. 2 (5), 388-393 (2001)
                                                                                                                                                                                                                                                                                                                  Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Winatoku, Tokyo 108-8639, Japan
Emali: ysuzuki@lams.u-kokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ch.T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,T., Suyama,A. and Sugano,S.
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Best Local Similarity 82.8%; Pred. No. 6.3e+05;
Matches 24; Conservative 0; Mismatches 5;
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/organism="Homo sapiens"
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AU102877.1 GI:13552398
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AU105237,1 GI:13554758
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BN397711 50 bp mRNA linear EST 17-JAN-2002 5009-0-35-H11.t.2 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
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2M02799R33F Mouse 10kb plasmid UUGC2M library Nus musculus genomic
clone UUGC2M0279E13 F, DNA sequence.
A2993993. GI:13865220
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1 (bases 1 to 50)

Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
'J. and Klöbutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
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/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SR+; Details on library
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."
/clone_lib="Sugano Homo sapiens cDNA library"
//note="Differential display comparison of untreated and
admethyliumarate treated U937 cells"
a 10 c 22 g 5 f
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1. Similarity 60.0%; Pred. No. 6.3e+05;
27; Conservative 0; Mismatches 18; Indels
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/etrain="CU428.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, 1L 60637, USA
                                                                                                                                                                                 Score 21; DB 9; I. Pred. No. 6.3e+05; 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
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ORGANISM

REFERENCE AUTHORS

JOURNAL TITLE

COMMENT

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/organism="Mus musculus"
/strain="C57BL/61"
/db_xref="Laxon:10090"
/clone=!ub-"wouse lokb plasmid UUGCIN library"
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/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42Nv; Purified genomic DNA from Mn
musculus C57BL/61 (male) was obtained from the Jackson
Laboratory Wouse DNA Resources/Soldocuments/dnares/). The DNA
was blunt ends in Parama velocity. The sheared DNA
was blunt end repaired with T DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar axcess The
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar axcess The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarces gel
electrophoracesis vector DNA was prepared from a derivative
of pWD42 (gil473114)ppla7129072.]), coop-runber
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLIO-Gold (Stratagane) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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AU106960 GI:13556481
                                             Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi.
Mammala; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musil.
[bases 1 to 48]
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacze, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouss whole genome scaffolding with paired end reads from 10kb
Dlasmid inserts
Chopplished (2000)
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Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: F column: 16
Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Robert B. Weiss
University of Uth Genome Center
University of Uth
Rm. 108, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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/note="Vector: PWD42nt, Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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48 bp DNA linear GSS 29-SEP-200
1M0026F16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0026F16 R, DNA sequence.
A2311362
A2311362.1 GI:10354248
GSS.
bouse mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 46)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ramil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
AM., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Welss, R.
                                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-*Nus musculus*
/strain="CS7Bu/65"
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/clone="Library"
/sox-*Female*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.24; Score 20.8; DB 17; Length 46; Best Local Similarity 70.04; Pred. No. 6.8e+05; Matches 28; Conservative 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 GATGAGAGTGGTGGTGGCGGCAGTGACCCTGGAGAGG 262
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0.279 row: E column: 13
Seg primer: CGTGTAAAACGACGCCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 46. Location/Qualifiers
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Bource

FEATURES

Gapa ö

LOCUS DEFINITION

RESULT 10 A2311362

ð 8 ACCESSION VERSION KEYWORDS SOURCE

BASE COUNT

ORIGIN

REFERENCE AUTHORS

MEDLINE COMMENT

FEATURES

JOURNAL

TITLE

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/Bak-TABLE.
/Jab_Note-"Vector: PMyd2nv; Purified genomic DNA from M. musculus C57BL/61 (male) was obtained from the Jackson Laboratory Morte-vector: PMyd2nv; Purified genomic DNA from M. musculus C57BL/61 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 7 DNA polymerase and T4 polymuclectide kinase. Adaptor ollygonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWHA2 (gil4732114|gb|x7129072.1), a copy-number inducable derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The shared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and slice C 20 g 10 t
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Mouse Whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Eukaryota, Netazoa: Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 45)
                                                                                                                                                                                /clone_lib="Mouse lokb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Natch
1.2%; Score 20.4; DB 17; Length 47;
Best Local Similarity 71.1%; Pred. No. 8.6e+05;
Matches 27; Conservative 0; Mismatches 11; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0268 row: F column: 01
Seq primer: CGTTGTARANGGACGAGT
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Context: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                               /db_xref-"taxon:10090"
/clone="UUGC1M0059H04"
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddurne
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A2985975
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                         Bukaryota; Metazoa; Chordata; Craniata; Vertchrata; Eutcleostomi; Nammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (160 12) (
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47 bp DNA linear GSS 29-SEP-2000 1M0059H04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0059H04 R, DNA sequence.

AZ331536

AZ331536.1 GI:10394326
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Bunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib-"Sugano Homo sapiens cDNA library"
/note-"Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
7 a 14 c 18 g 11 t
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Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: H column: 04
Seg primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             922 CTGTTCCAGCTCCTCGTGGCCTGGCCTACTGCCA 956
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/organism-"Homo saplens"
/db_xref-"taxon:9606"
/clone-"CAS09689"
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Context: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yutaka Suzuki
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Fax: 801 585 7177
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A2331536/c
LOCUS
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ð 셤 REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

Gaps

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AI475974

L196D06 x1 NCI_CGAP_COl4 Homo sapiens CDNA clone IMAGE:2154899 3'
similar to TR:Q17352 Q17352 REM-TYPE RNA BINDING PROTEIN. ; contains element MSRI repetitive element ;, mRNA sequence.

AI475974

AI475974.1 GI:4329019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Warron's Cane Index Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs rémail.inh.gov

Tissue Procurement: Christopher Moskaluk, N.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Grag Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NII-CGAP clone distribution information can be found through the I.N.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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Eukaryota: Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 1.2%; Score 20.2; DB 9; Length 49; Local Similarity 75.8%; Pred. No. 9.9e+05; Local 25; Conservative 0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1156 ATGIGGGTGTGGGCTGCATCTTCTATGAGATG 1188
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/db_xref-"taxon:9606"
/clone-"IMAGE:2154899"
/clone_lib-"NCI_CGAP_CO14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 ATGGGGTGTGTGAGCTGCATGTGCTCTGTGCTG 1
                                                                         /organism-"Mus musculus"
                                                                                                                                                                                             /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH108"
         High quality sequence stop: 1. Location/Qualifiers
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                           FEATURES
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                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sclurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 49)
Marra, M., Hillacri, Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Rucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Noore, B., Theising, B., Wille, T., Lennon, G., Soares, B., Milson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA204601 49-FEB-1997 mu25c05.rl Scares_thymus_2NbWT Wus musculus cDNA clone IMAGE:6404245' similar to SW:143G_BOVIN P29359 14-3-3 PROTEIN GAMMA ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the MAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                  /db_aref-"taxon:10090"
/clone-fugGCAM0268F01'
/clone_lib-Mouse lOkb plasmid UGGCAM library"
/sex-"Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marta M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.2%; Score 20.2; DB 17; Length 45; Best Local Similarity 68.3%; Pred. No. 9.5e+05; Matches 28; Conservative 0; Mismatches 13; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seg primer: -28M13 rgv2 from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
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AA204601.1 GI:1800608
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source
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AA204601/c
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AUTHORS
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/Lissue_type="moderately-differentiated adenocarcinoma" /lab.host="DNIOB" /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sali; Site_2: NOCI: Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Life Technologies catalog #: 11531-019" a 13 c 14 g 4 t
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BASE COUNT ORIGIN

Gapa ö Ouery Match
Best Local Similarity 72.2%; Pred. No. 1e+06;
Matches 26; Conservative 0; Mismatches 10; Indels

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Search completed: March 4, 2003, 00:50:32 Job time : 2635 secs